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PULLULANASE VARIANTS AND METHODS FOR PREPARING SUCH VARIANTS WITH PREDETERMINED PROPERTIES

FIELD OF THE INVENTION

The present invention relates to variants of pullulanases and to methods for constructing such variants with altered properties, including stability (e.g., thermostability), pH dependent activity, substrate specificity, such as increased isoamylase activity, or specific activity; specific activity at a given pH and/or altered substrate specificity, such as an altered pattern of substrate cleavage or an altered pattern of substrate inhibition.

BACKGROUND OF THE INVENTION

Starches such as corn, potato, wheat, manioc and rice starch are used as the starting material in commercial large-scale production of sugars, such as high fructose syrup, high maltose syrup, maltodextrins, amylose, G4-G6 oligosaccharides and other carbohydrate products such as fat replacers.

Degradation of starch

Starch usually consists of about 80% amylopectin and 20% amylose. Amylopectin is a branched polysaccharide in which linear chains alpha-1,4 D-glucose residues are joined by alpha-1,6 glucosidic linkages. Amylopectin is partially degraded by alpha-amylase, which hydrolyzes the 1,4-alpha-glucosidic linkages to produce branched and linear oligosaccharides. Prolonged degradation of amylopectin by alpha-amylase results in the formation of so-called alpha-limit dextrins that are not susceptible to further hydrolysis by the alpha-amylase. Branched oligosaccharides can be hydrolyzed into linear oligosaccharides by a debranching enzyme. The remaining branched oligosaccharides can be depolymerized to D-glucose by glucoamylase, which hydrolyzes linear oligosaccharides into D-glucose.

Amylose is a linear polysaccharide built up of D-glucopyranose units linked together by alpha-1,4 glucosidic linkages. Amylose is degraded into shorter linear

oligosaccharides by alpha-amylase, the linear oligosaccharides being depolymerized into D-glucose by glucoamylase.

In the case of converting starch into a sugar, the starch is depolymerized. The depolymerization process consists of a pretreatment step and two or three consecutive process steps, namely a liquefaction process, a saccharification process and, depending on the desired end product, optionally an isomerization process.

Pre-treatment of native starch

Native starch consists of microscopic granules that are insoluble in water at room temperature. When an aqueous starch slurry is heated, the granules swell and eventually burst, dispersing the starch molecules into the solution. During this "gelatinization" process there is a dramatic increase in viscosity. As the solids level is 30-40% in a typical industrial process, the starch has to be thinned or "liquefied" so that it can be handled. This reduction in viscosity is today mostly obtained by enzymatic degradation.

Liquefaction

During the liquefaction step, the long-chained starch is degraded into smaller branched and linear units (maltodextrins) by an alpha-amylase (*e.g.*, Termamyl™, available from Novozymes A/S, Denmark). The liquefaction process is typically carried out at about 105-110°C for about 5 to 10 minutes followed by about 1-2 hours at about 95°C. The pH generally lies between about 5.5 and 6.2. In order to ensure optimal enzyme stability under these conditions, calcium is added, e.g., 1 mM of calcium (40 ppm free calcium ions). After this treatment the liquefied starch will have a "dextrose equivalent" (DE) of 10-15.

Saccharification

After the liquefaction process the maltodextrins are converted into dextrose by addition of a glucoamylase (e.g. AMG™, available from Novozymes A/S) and a debranching enzyme, such as an isoamylase (see, e.g., US Patent No. 4,335,208) or a pullulanase (*e.g.*, Promozyme®, available from Novozymes A/S;

see US Patent No. 4,560,651). Before this step the pH is reduced to a value below 4.5, e.g. about 3.8, maintaining the high temperature (above 95°C) for a period of, e.g., about 30 min. to inactivate the liquefying alpha-amylase to reduce the formation of short oligosaccharides called "panose precursors" which cannot be hydrolyzed properly by the debranching enzyme.

The temperature is then lowered to 60°C, glucoamylase and debranching enzyme are added, and the saccharification process proceeds for about 24-72 hours.

Normally, when denaturing the alpha-amylase after the liquefaction step, a small amount of the product comprises panose precursors, which cannot be degraded by pullulanases or AMG. If active amylase from the liquefaction step is present during saccharification (i.e., no denaturing), this level can be as high as 1-2% or even higher, which is highly undesirable as it lowers the saccharification yield significantly. For this reason, it is also preferred that the alpha-amylase is one which is capable of degrading the starch molecules into long, branched oligosaccharides (such as, e.g., the Fungamyl™-like alpha-amylases) rather than shorter branched oligosaccharides.

Isomerization

When the desired final sugar product is, e.g., high fructose syrup, the dextrose syrup may be converted into fructose by enzymatic isomerization. After the saccharification process the pH is increased to a value in the range of 6-8, preferably about pH 7.5, and the calcium is removed by ion exchange. The dextrose syrup is then converted into high fructose syrup using, e.g., an immobilized glucose isomerase (such as Sweetzyme™, available from Novozymes A/S).

Debranching enzymes

Debranching enzymes which can attack amylopectin are divided into two classes: isoamylases (E.C. 3.2.1.68) and pullulanases (E.C. 3.2.1.41), respectively. Isoamylase hydrolyses alpha-1,6-D-glucosidic branch linkages in amylopectin and beta-limit dextrins and can be distinguished

from pullulanases by the inability of isoamylase to attack pullulan, and by their limited action on alpha-limit dextrins.

When an acidic stabilized alpha-amylase is used for the purpose of maintaining the amylase activity during the entire saccharification process (no inactivation), the degradation specificity should be taken into consideration. It is desirable in this regard to maintain the alpha-amylase activity throughout the saccharification process, since this allows a reduction in the amyloglucidase addition, which is economically beneficial and reduces the AMG™ condensation product isomaltose, thereby increasing the DE (dextrose equivalent) yield.

It will be apparent from the above discussion that the known starch conversion processes are performed in a series of steps, due to the different requirements of the various enzymes in terms of, e.g., temperature and pH. It would therefore be desirable to be able to engineer one or more of these enzymes, e.g., pullulanases, so that the overall process could be performed in a more economical and efficient manner. One possibility in this regard is to engineer the otherwise thermolabile pullulanases so as to render them more stable at higher temperatures.

BRIEF DISCLOSURE OF THE INVENTION

The inventors have modified the amino acid sequence of a pullulanase to obtain variants with improved properties, based on the three-dimensional structure of the pullulanase Promozyme® (available from Novozymes A/S, Denmark). The variants have altered physicochemical properties, e.g., an altered pH optimum, improved thermostability, increased specific activity or an altered cleavage pattern.

Accordingly, the object of the present invention is to provide a method for constructing pullulanases having altered properties, in particular to provide a method for constructing pullulanases having improved thermostability, altered pH dependent activity and/or altered substrate specificity, such as increased isoamylase activity.

Thus, in its broadest aspect, the present invention relates to a method for constructing a variant of a parent

pullulanase, wherein the variant has at least one altered property as compared to said parent pullulanase, which method comprises:

i) analyzing the structure of the pullulanase to identify, on the basis of an evaluation of structural considerations, at least one amino acid residue or at least one structural region of the pullulanase, which is of relevance for altering said property;

ii) constructing a variant of the pullulanase, which as compared to the parent pullulanase, has been modified in the amino acid residue or structural part identified in i) so as to alter said property; and

iii) testing the resulting pullulanase variant for said property.

The property that may be altered by the above methods of the present invention may be, e.g., thermostability, pH dependent activity, specific activity, or substrate specificity. Thus, the variant may have, e.g., increased thermostability, higher activity at a lower pH, an altered pH optimum, improved thermostability, or increased specific activity, such as increased isoamylase activity.

Although it has been described in the following that modification of the parent pullulanase in certain regions and/or positions is expected to confer a particular effect to the thus produced pullulanase variant (such as an improved thermostability or an increased isoamylase activity), it should be noted that modification of the parent pullulanase in any of such regions may also give rise to any other of the above-mentioned effects. For example, any of the regions and/or positions mentioned as being of particular interest with respect to, e.g., improved thermostability, may also give rise to, e.g., higher activity at a lower pH, an altered pH optimum, or increased specific activity, such as increased isoamylase activity.

Further aspects of the present invention relates to variants of a pullulanase, the DNA encoding such variants and methods of preparing the variants. Still further aspects of the present invention relates to the use of the variants for

various industrial purposes, in particular for processes where sweeteners are made from starch. Other aspects of the present invention will be apparent from the below description as well as from the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the DNA plasmid pCA36 harboring the gene encoding the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3).

APPENDIX 1 shows the structural coordinates for the solved crystal structure of Promozyme®

APPENDIX 2 shows a sequence alignment between Promozyme® (SEQ ID NO: 2), the pullulanase from *Bacillus deramificans* (SEQ ID NO: 4), and the pullulanase from *Bacillus acidopullulyticus* (SEQ ID NO: 6) described in FEMS Mic. Let. (1994) 115, 97-106.

DETAILED DISCLOSURE OF THE INVENTION

Pullulanases

As explained above, pullulanases are enzymes classified in EC 3.2.1.41 and such enzymes are characterized by their ability to hydrolyze the alpha-1,6-glycosidic bonds in, for example, amylopectin and pullulan.

A particularly interesting pullulanase is the pullulanase from *Bacillus acidopullulyticus* described in US 4,560,651 (hereinafter referred to as Promozyme®). Promozyme® has the amino acid sequence set forth in amino acids 1-921 of SEQ ID NO: 1. The three-dimensional structure of Promozyme® is described below.

Another interesting pullulanase is the pullulanase from *Bacillus deramificans* described in US 5,736,375. This enzyme has the amino acid sequence set forth in amino acid sequence 1-928 of SEQ ID NO: 3. Homology building of the tree-dimensional structure of the above-mentioned pullulanase is described below.

In general, a preferred pullulanase suitable for the purpose described herein should have one or more of the following properties:

i) A three-dimensional structure homologous to Promozyme®.

ii) An amino acid sequence which is at least 40% homologous to SEQ ID NO: 1 or SEQ ID NO: 3, preferably at least 50%, e.g., at least 60%, such as a least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homologous to SEQ ID NO:1 or SEQ ID NO: 3.

iii) A nucleic acid sequence which hybridizes to the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:3.

The structural homology referred to above in i) above is based on other sequence homologies, hydrophobic cluster analysis or by reverse threading (Huber, T ; Torda, AE, PROTEIN SCIENCE Vol. 7 , No. 1 pp. 142-149 (1998)) and which by any of these methods is predicted to have the same tertiary structure

as Promozyme®, wherein the tertiary structure refers to the overall folding or the folding of Domains N1, N2, A, B, and C. Alternatively, a structural alignment between Promozyme® and homologous sequences may be used to identify equivalent positions.

For example, the homology between various pullulanase with known amino acid sequence has been compiled in the below matrix:

	1	2	3	4	5	6	7	8	9	10
1. pula_kleae	100	86	59	51	52	53	52	52	55	50
2. pula_klepn		100	58	51	51	53	53	53	53	52
3. w81973			100	55	56	52	55	54	51	56
4. r56989				100	98	60	76	54	56	76
5. sp929mat					100	61	78	54	57	78
6. fervido_x						100	61	57	54	62
7. sp734							100	56	54	91
8. r71616								100	54	56
9. w09257									100	54
10. Promozyme®										100

1. Pula_kleae: Pullulanase from *Klebsiella aerogenes* (*J. Bacteriol.* (1987) 169, 2301-2306).

2. Pula_klepn: Pullulanase from *Klebsiella pneumonia* (*Mol. Microbiol.* (1990) 4, 73-85; *J. Bacteriol.* (1985) 164, 639-645; *J. Bacteriol.* (1989) 171, 3673-3679).

3. W81973: Pullulanase fragment from zea mays (WO 98/50562).

4. r56989: Mature pullulanase from *Bacillus deramificans* T 89.117D (EP 0 605 040).

5. sp929mat: Mature part of pullulanase from *Bacillus deramificans* (US Patent 5,736,375).

6. fervido_x: Mature part of pullulanase from *Fervidobacterium pennavorans* Ven5 (*Appl. Environ. Microb.* (1997) 63, 1088-1094).

7. sp734: Mature pullulanase from *Bacillus acidopullulyticus* (*FEMS Mic. Let.* (1994) 115, 97-106.

8. r71616: Pullulanase from *Thermus sp.* (JP 07023783).

9. w09257: Pullulanase from *Bacillus sp.* KSM-AP 1378 (WO 96/35794).

The above homology calculations were determined by use of the GAP program from the UWGCG package using default values for GAP penalties, i.e., GAP creation penalty of 3.0 and GAP extension penalty of 0.1 (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711).

A sequence alignment between Promozyme® (SEQ ID NO: 1), the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) and the pullulanase from *Bacillus acidopullulyticus* (SEQ ID NO: 5) described in FEMS Mic. Let. (1994) 115, 97-106, is shown in Appendix 2.

Three-dimensional structure of pullulanase

Promozyme® was used to elucidate the three-dimensional structure forming the basis for the present invention.

The structure of Promozyme® was solved in accordance with the principle for x-ray crystallographic methods, for example, as given in X-Ray Structure Determination, Stout, G.K. and Jensen, L.H., John Wiley & Sons, Inc. NY, 1989.

The structural coordinates for the solved crystal structure of Promozyme® using the isomorphous replacement method are given in standard PDB format (Protein Data Bank, Brookhaven National Laboratory, Brookhaven, CT) as set forth in Appendix 1. It is to be understood that Appendix 1 forms part of the present application. In the context of Appendix 1, the following abbreviations are used: WAT refers to water or to calcium. Amino acid residues are given in their standard three-letter code.

The structure of said Pullulanase is made up of five globular domains, ordered N1 being 1-310 (which may be subdivided into N1' being residues 1-111, N1''being residues 112-158 and 261-310, and N1''' being residues 159-261), N2, A, B, and C. The domains can be defined as being residues 1-310 for domain N1, 311-420 for Domain N2, residues 421-556 and 596-835 for domain A, residues 557-595 for Domain B, residues 596-922 for Domain C, wherein the numbering refers to the amino

acid sequence in SEQ ID NO: 1. Features of Domains N1, A, B and C of particular interest are described below.

Domain N1

Domain N1 contains in this particular pullulanase an extra loop of 100 residues compared to the pullulanase from *Bacillus acidopullulyticus* having the amino acid sequence shown in SEQ ID NO: 5. The loop is also present in the pullulanase from *Bacillus deramificans* having the amino acid sequence shown in SEQ ID NO: 3.

Part of the N2 domain is homologeous to the N1 domain of *Pseudomonase amyloderamosa* isoamylase (1bf2.pdb from Brookhaven database).

Domain A

Domain A is the largest domain and contains the active site which comprises a cluster of three amino acid residues, D622, D736 and E651, spatially arranged at the bottom of a cleft in the surface of the enzyme. The structure of Domain A shows an overall fold in common with the alpha-amylases for which the structure is known, viz. the (beta/alpha) 8 barrel with eight central beta strands (numbered 1-8) and eight flanking alpha-helices. The beta-barrel is defined by McGregor, *J. Prot. Chem.* 7:399, 1988. The C-terminal end of the beta strand 1 is connected to helix 1 by a loop denoted loop 1 and an identical pattern is found for the other loops, although the loops show some variation in size and some can be quite extensive.

The eight central beta-strands in the (beta/alpha) 8 barrel superimpose reasonably well with the known structures of family 13 (Henrissat B. *Biochem. J.* (1991) 280, 309-316 and Henrissat B. and Bairoch A. *Biochem. J.* (1993) 293, 781-788). This part of the structure, including the close surroundings of the active site located at the C-terminal end of the beta-strands, shows a high degree of homology with isoamylases.

In contrast, the loops connecting the beta-strands and alpha helices display a high degree of variation from the known structures of family 13 enzymes. These loops constitute the

structural context of the active site, and the majority of the contacts to the substrate are found among residues located in these loops. Distinguishing characteristics such as substrate specificity, substrate binding, pH activity profile, substrate cleavage pattern, and the like, are determined by specific amino acids and the positions they occupy in these loops.

Domain B

Domain B, also referred to as loop 3 of the (beta/alpha) 8 barrel, in comprises amino acid residues 557-595 of the amino acid sequence shown in SEQ ID NO: 1. The most striking difference to other family 13 enzymes is the short amino acid sequence. This short sequence loop are of the same size as the isoamylase loop 3 and spatially positioned close to the active site residues and in close contact to the substrate.

Domain C

Domain C in Promozyme® comprises amino acid residues 596-922 of the amino acid sequence shown in SEQ ID NO: 1. Domain C is composed entirely of beta-strands which form a single 8-stranded sheet structure that folds back on itself, and thus may be described as a beta-sandwich structure. One part of the beta-sheet forms the interface to Domain A.

Substrate Binding Site

Parts of the loop discussed above in the context of domains A, B and N2 are of particular interest for substrate interaction and active site reactivity. In particular, in domain A, residues 439-443 in loop 1, residues 490-514 in loop 2, residues 621-628 in loop 4, residues 652-668 in loop 5, residues 679-694 in loop 6, residues 733-740 in loop 7 and residues 787-796 in loop 8; in domain B, residues 553-564 and 581-592 in loop 3; in domain N2, residues 400-404, wherein residue positions correspond to the amino acids in the amino acid sequence in SEQ ID NO: 1.

Homology building of *Bacillus d ramificans* pullulanase or other pullulanases.

The structure of the *Bacillus deramificans* pullulanase (SEQ ID NO: 3) was model built on the structure disclosed in Appendix 1 herein. The structure of other pullulanases may be built analogously.

A model structure of a pullulanase can be built using the Homology program or a comparable program, e.g., Modeller (both from Molecular Simulations, Inc., San Diego, CA). The principle is to align the sequence of the pullulanase with the known structure with that of the pullulanase for which a model structure is to be constructed. The structurally conserved regions can then be built on the basis of consensus sequences. In areas lacking homology, loop structures can be inserted, or sequences can be deleted with subsequent bonding of the necessary residues using, e.g., the program Homology. Subsequent relaxing and optimization of the structure should be done using either Homology or another molecular simulation program, e.g., CHARMm from Molecular Simulations.

Methods for designing novel pullulanase variants

In a first aspect the present invention relates to a method for producing a variant of a parent pullulanase, wherein the variant has at least one altered property as compared to the parent pullulanase, the method comprising:

i) modeling the parent pullulanase on the three-dimensional structure of SEQ ID NO: 1 depicted in Appendix 1 to produce a three-dimensional structure of the parent pullulanase;

ii) identifying in the three-dimensional structure obtained in step (i) at least one structural part of the parent pullulanase, wherein an alteration in the structural part is predicted to result in an altered property;

iii) modifying the nucleic acid sequence encoding the parent pullulanase to produce a nucleic acid sequence encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to the structural part; and

iv) expressing the modified nucleic acid sequence in a host cell to produce the variant pullulanase.

Structural part

The structural parts which is identified in step ii) of the method of the invention may be composed of one amino acid residue. Normally, however, the structural part comprises more than one amino acid residue, typically constituting one of the above-mentioned parts of the pullulanase structure such as one of the N1, N2, A, B, or C domains, an interface between any of these domains, a calcium binding site, a loop structure, the substrate binding site, or the like.

The structural or functional considerations may involve an analysis of the relevant structure or structural part and its contemplated impact on the function of the enzyme. For example, an analysis of the functional differences between pullulanases and the various isoamylases may be used for assigning certain properties of Promozyme® or homologeous model builded structure to certain parts of the Promozyme® or homologeous model build structure or to contemplate such relationship. For instance, differences in the pattern or structure of loops surrounding the active site may result in differences in access to the active site of the substrate and thus differences in substrate specificity and/or cleavage pattern.

Furthermore, parts of a pullulanase involved in substrate binding, and thus, for example, substrate specificity and/or cleavage, thermostability, and the like, have been identified (*vide infra*).

The modification of an amino acid residue or structural region is typically accomplished by suitable modifications of a nucleic acid sequence encoding the parent enzyme in question. The modification may be substitution, deletion or insertion of an amino acid residue or a structural part.

The property to be modified may be stability (e.g., thermostability), pH dependent activity, substrate specificity, such as decreased condensation reactions, isoamylase like activity etc. Thus, the altered property may be an altered specific activity at a given pH and/or altered substrate specificity, such as an altered pattern of substrate cleavage or an altered pattern of substrate inhibition.

In step ii) of the method according to the invention the part of the structure to be identified is preferably one which in the folded enzyme is believed to be in contact with the substrate (cf. the disclosure above in the section entitled "Substrate Binding Site") or involved in substrate specificity and/or cleavage pattern, and/or one which is contributing to the pH or temperature profile of the enzyme, or is otherwise responsible for the properties of the pullulanase.

Described in the following are specific types of variants that have been designed by use of the method of the invention.

The variants of the invention may comprise additional modifications in addition to the modifications described herein. The variants preferably have an amino acid sequence having more than 40% homology with SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5, preferably more than 50%, e.g., more than 60%, such as more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 91%, more than 92%, more than 93%, more than 94%, more than 95%, more than 96%, more than 97%, more than 98% or more than 99% homology with the amino acid sequences shown in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5.

In the present context the term "homologous to" or "homology" (also sometimes referred to as "similarity") is used in it conventional meaning and the "homology" between two amino acid sequences may be determined by use of any conventional algorithm, preferably by use of the GAP program from the UWGCG package using default values for GAP penalties, i.e. GAP creation penalty of 3.0 and GAP extension penalty of 0.1 (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711). The method is also described in S.B. Needleman and C.D. Wunsch, *Journal of Molecular Biology*, 48, 443-445 (1970).

Alternative methods of designing pullulanase variants

The three-dimensional structure of a pullulanase is influenced by the presence (or absence) of the structural spatial location of ions, such as especially calcium ion (also

sodium ions may be present). Such information may be used as a parameter when designing a pullulanase variant based on informations extracted from one parent pullulanase.

In one embodiment of the invention the parent pullulanase is characterized by having calcium ion(s) in the structure.

A specific example of such parent pullulanase is *Klebsiella sp.* mentioned above.

In another embodiment of the invention the parent pullulanase is a pullulanase which do not have metal ion(s) in the structure, in particular calcium(s) ions.

A specific example of a parent pullulanase which do not have metal ion(s) in the structure is PROMOZYME®

In general, informations in respect of structural parts (as defined below) and/or structural elements, e.g., metal ions present in the three-dimensional structure of a parent pullulanase, may be used for as a parameter when model building other corresponding parent pullulanases having, e.g., metal ion(s) in corresponding fixed spatially location(s).

A parent pullulanase may have from no ions to one or more ions in the structure, typically calcium and/or sodium ions. Parent pullulanases having spatially similar located ions (as a solved three-dimensional structure) will also spatially have a similar three dimensional structure. This means that modeling of such a corresponding parent pullulanase with spatially fix ion(s) corresponding to that of, e.g., Promozyme® (disclosed in Appendix 1), said corresponding parent pullulanase having at least 50% homology in the primary structure (as defined above) when compared to SEQ ID NO: 1, 3, or 5, may according to the invention be carried out as described below. If said corresponding parent pullulanase has at least 60%, or at least 70%, at least 80%, or at least 90% homology in the primary structure when compared to SEQ ID NO: 1, 3, or 5, the modeling will be even more precise.

Thus, in an aspect the invention relates to a method of producing a variant of a parent pullulanase having an altered property relative to the parent pullulanase, wherein the parent pullulanase has the sequence of SEQ ID Nos: 2, 4, 6, or has a

sequence homology of at least 40% to the sequence of SEQ ID NO: 2, 4, or 6, said method comprising

(a) identifying in the three-dimensional structure depicted in Appendix 1 at least one structural part wherein an alteration in a corresponding structural part in said parent pullulanase is predicted to result in an altered property; wherein the altered property is selected from the group consisting of thermostability, pH dependent activity, substrate specificity, isoamylase like activity, specific activity, altered pattern of substrate cleavage, or an altered pattern of substrate inhibition;

(b) modifying the sequence of a nucleic acid encoding the parent pullulanase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

(d) expressing the modified nucleic acid in a host cell to produce the variant pullulanase;

wherein the variant has alpha-amylase enzymatic activity and has at least one altered property relative to the parent.

Alternatively, the invention relates to a method of producing a variant of a parent pullulanase having an altered property relative to the parent pullulanase, wherein the parent pullulanase has the sequence of SEQ ID Nos: 2, 4, or 6, or has a sequence homology of at least 40 % to the sequence of SEQ ID NO: 2, 4, or 6, said method comprising

(a1) providing a three-dimensional pullulanase structure that consists of one or more of domains N1 , N2, A, B, and C, in particular N1'';

(a2), do or do not contain one or more metal ions, in particular calcium or sodium ion(s), in the structure;

(a3) a three dimensional structure corresponding/equivalent to the three dimensional structure in shown in APPENDIX 1, one or more of the above mentioned domains;

(b) identifying in the three-dimensional structure at least one structural part of the parent wherein an alteration in said structural part or corresponding structural part in

said parent pullulanase is predicted to result in said altered property and wherein said altered property is selected from the group consisting of thermostability, pH dependent activity, substrate specificity, isoamylase like activity, specific activity, altered pattern of substrate cleavage, or an altered pattern of substrate inhibition;

(c) modifying the sequence of a nucleic acid encoding the parent pullulanase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

(d) expressing the modified nucleic acid in a host cell to produce the variant alpha-amylase,

wherein the variant has alpha-amylase enzymatic activity and has at least one altered property relative to the parent.

In an embodiment the parent pullulanase consists of domains N1'', N2, A, B, and C.

In an embodiment the parent pullulanase consists of domains N1', N2, A, B, and C.

In an embodiment the parent pullulanase consists of domains N2, A, B, and C.

In an embodiment the parent pullulanase consists of domains N1', N1'', N2, A, B, and C.

In an embodiment the parent pullulanase consists of domains N1'', N1''', N2, A, B, and C.

Properties to be modified

As mentioned above, the property to be modified may be stability (e.g., thermostability), pH dependent activity, substrate specificity, such as increased isoamylase activity, or specific activity. Thus, the altered property may be an altered specific activity at a given pH and/or altered substrate specificity, such as an altered pattern of substrate cleavage or an altered pattern of substrate inhibition.

In a particular interesting embodiment of the invention the property to be modified is the thermostability of the enzyme.

Common structural elements

Common structural elements referred to in vi) means elements involved in keeping the three dimensional structure of the enzyme, e.g., metal ions in the structure etc.

Thermostability

In the present context, the term "thermostable" (or "thermostability") refers in general to the fact that the pullulanase variants according to the invention have an improved thermostability compared to the relevant parent pullulanase. The degree of improvement in thermostability can vary according to factors such as the thermostability of the parent pullulanase and the intended use of the pullulanase variant, i.e., whether it is primarily intended to be used for liquefaction or for saccharification or both. It will be apparent from the discussion below that for saccharification, the enzyme variant should maintain a substantial degree of enzyme activity during the saccharification step at a temperature of at least about 63°C, preferably at least about 70°C, while an enzyme variant designed for use in the liquefaction step should be able to maintain a substantial degree of enzyme activity at a temperature of at least about 95°C.

The improved thermostability of enzyme variants according to the invention can in particular be defined according to one or more of the following criteria:

In one embodiment, the pullulanase variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostabilty) as defined by differential scanning calorimetry (DSC) using the method described herein.

In another embodiment, the pullulanase variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostabilty) as defined by an increased half-time ($T_{1/2}$) of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about

100%, in the "$T_{1/2}$ assay for liquefaction" described herein, using a pH of 5.0 and a temperature of 95°C. Pullulanase variants according to this definition are suitable for use in the liquefaction step of the starch conversion process.

Alternatively or additionally, a pullulanase variant suitable for use in liquefaction can be defined as having an improved thermostability as defined by an increased residual enzyme activity of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "assay for residual activity after liquefaction" described herein, using a pH of 5.0 and a temperature of 95°C.

In a further embodiment, the enzyme variant of the invention has an improved thermostability (and/or the method of the invention provides a pullulanase with an improved thermostabilty) as defined by an increased half-time ($T_{1/2}$) of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "$T_{1/2}$ assay for saccharification" described herein, using a pH of 4.5 and a temperature of 70°C. Such variants are suitable for use in the saccharification step of the starch conversion process.

Alternatively or additionally, a pullulanase variant suitable for saccharification can be defined as having an improved thermostability as defined by an increased residual enzyme activity of at least about 5%, preferably at least about 10%, more preferably at least about 15%, more preferably at least about 25%, most preferably at least about 50%, such as at least about 100%, in the "assay for residual activity after saccharification" described herein, using a pH of 4.5 and a temperature of 63°C. Preferably, this improved thermostability is also observed when assayed at a temperature of 70°C.

The term "substantially active" as used herein for a given pullulanase variant and a given set of conditions of temperature, pH and time means that the relative enzymatic activity of the enzyme variant is at least about 25%,

preferably at least about 50%, in particular at least about 60%, especially at least about 70%, such as at least about 90% or 95%, e.g., at least about 99% compared to the relative activity of the parent enzyme tested under the same set of conditions.

One advantage of the thermostable pullulanase of the invention is that they make it possible to perform liquefaction and debranching simultaneously before the saccharification step. This has not previously been possible, since the known pullulanases with acceptable specific activity are thermolabile and are inactivated at temperatures above 60°C. (Some thermostable pullulanases from *Pyrococcus* are known, but these have an extremely low specific activity at higher temperatures and are thus unsuitable for purposes of the present invention). By debranching, using the thermostable pullulanases of the invention, during liquefaction together with the action of an alpha-amylase, the formation of panose precursors is reduced, thereby reducing the panose content in the final product and increasing the overall saccharification yield. It is also possible in this manner to extend the liquefaction process time without risking formation of large amount of panose precursors. By prolonging the liquefaction step, the DE yield is increased from 10-15 to, e.g., 15-20, reducing the need for glucoamylase. This reduced glucoamylase requirement is in turn advantageous as the formation of undesired isomaltose is reduced, thereby resulting in an increased glucose yield. In addition, the reduced glucoamylase addition enables the saccharification step to be carried out at a higher substrate concentration (higher DS, dry substances, concentration) than the normal approx. 30-35% used according to the prior art. This allows reduced evaporation costs downstream, e.g., in a high fructose corn syrup process, and the saccharification reaction time can also be reduced, thereby increasing production capacity. A further advantage is that alpha-amylase used in the liquefaction process does not need to be inactivated/denatured in this case.

Furthermore, it is also possible to use the thermostable pullulanases of the invention during saccharification, which is advantageous for several reasons. In the conventional starch

saccharification process, the process temperature is not more than 60°C due to the fact that neither the saccharification enzyme pullulanase nor AMG™ (i.e., glucoamylase) are sufficiently thermostable to allow the use of a higher temperature. This is a disadvantage, however, as it would be very desirable to run the process at a temperature of above about 60°C, in particular above 63°C, e.g. about 70°C, to reduce microbial growth during the relatively long saccharification step. Furthermore, a higher process temperature normally gives a higher activity per mg of enzyme (higher specific activity), thereby making it possible to reduce the weight amount of enzyme used and/or obtain a higher total enzymatic activity. A higher temperature can also result in a higher dry matter content after saccharification, which would be beneficial in terms of reducing evaporation costs.

In another interesting embodiment of the invention the property to be modified is the substrate specificity of the pullulanase, in particular to modify the substrate specificity of the pullulanase in such a way the variant pullulanase becomes more "isoamylase-like" in the sense of having an increased activity towards high molecular weight branched starchy material such as glycogen and amylopectin. Methods for determining the substrate specificity of pullulanases are discussed in the following section entitled "Methods for determining stability, activity and specificity".

Thus, when used herein, the term "increased isoamylase activity" refers in general to the fact that the pullulanase variants according to the invention exhibits a higher activity towards high molecular weight branched starchy material, such as glycogen and amylopectin as compared to the parent pullulanase.

The increased isoamylase activity of the pullulanase variants according to the invention can in particular be defined according to the below criteria:

In one embodiment the pullulanase variant according to the invention has an increased isoamylase activity as defined by an increase of at least 5%, preferably of at least 10%, more preferably of at least 15%, more preferably of at least 25%,

most preferably of at least 50%, in particular of at least 75%, such as of at least 100% in the number of reducing ends formed in the "assay for isoamylase-like activity" described herein, using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature of 60°C and when incubated with a 10 w/v rabbit liver glycogen solution for a period of 10 min.

In the present context the term "pullulanase activity" is intended to mean that the pullulanase variant in question is capable of degrading pullulan when tested as described in the Examples (see the section entitled "Determination of pullulanase activity).

Methods for determining stability, activity and specificity

Thermostability

Thermostability Assay 1

Thermostability of pullulanase variants of the invention may be detected by measuring the residual activity by incubating the enzyme under accelerated stress conditions, which comprise: pH 4.5 in a 50 mM sodium acetate buffer without a stabilizing dextrin matrix (such as the approximately 35% dry matter which is normally present during saccharification). The stability can be determined at isotherms of, e.g., 63°C, 70°C, 80°C, 90°C and 95°C, measuring the residual activity of samples taken from a water bath at regular intervals (e.g. every 5 or 10 min.) during a time period of 1 hour. For determining stability for the purpose of liquefaction, a pH of 5.0, a temperature of 95°C and a total assay time of 30 to 120 minutes are used ("assay for residual activity after liquefaction"). For determining stability for the purpose of saccharification, a pH of 4.5, a temperature of 63°C or 70°C and a total assay time of 30 minutes are used ("assay for residual activity after saccharification").

Thermostability Assay 2 ($T_{1/2}$)

Alternatively, the thermostability of pullulanase variants of the invention may be expressed as a "half-time" ($T_{1/2}$), which

is defined as the time, under a given set of conditions, at which the activity of the enzyme being assayed is reduced to 50% of the initial activity at the beginning of the assay. In this case, the "$T_{1/2}$ assay for liquefaction" uses a pH of 5.0 and a temperature of 95°C, while the "$T_{1/2}$ assay for saccharification" uses a pH of 4.5 and a temperature of 70°C. The assay is otherwise performed as described above for the respective assays for residual activity.

Activity: Somogyi-Nelson method for determination of reducing sugars

The activity of pullulanases can be measured using the Somogyi-Nelson method for the determination of reducing sugars (*J. Biol. Chem.* 153, 375 (1944)). This method is based on the principle that sugar reduces cupric ions to cuprous oxide, which reacts with an arsenate molybdate reagent to produce a blue colour that is measured spectrophotometrically. The solution to be measured must contain 50-600 mg of glucose per liter. The procedure for the Somogyi-Nelson method is as follows:

Sample value: Pipet 1 ml of sugar solution into a test tube. Add 1 ml of copper reagent. Stopper the test tube with a glass bead. Place the test tube in a boiling water bath for 20 minutes. Cool the test tube. Add 1 ml of Nelson's color reagent. Shake the test tube without inverting it. Add 10 ml of de-ionized water. Invert the test tube and shake vigorously. Measure the absorbance at 520 nm, inverting the test tube once immediately prior to transfer of the liquid to the cuvette.

Blank value: Same procedure as for the sample value, but with water instead of sugar solution.

Standard value: Same procedure as for the sample value.

<u>Calculations:</u> In the region 0-2 the absorbance is proportional to the amount of sugar.

$$\text{mg sugar/l} = \frac{100\ (\text{sample} - \text{blank})}{(\text{standard} - \text{blank})}$$

$$\%\ \text{glucose} = \frac{(\text{sample} - \text{blank})}{}$$

100 x (standard - blank)

Reagents:

1. Somogyi's copper reagent

35.1 g $Na_2HPO_4.2H_2O$ and 40.0 g potassium sodium tartrate ($KNaC_4H_4O_2.4H_2O$) are dissolved in 700 ml of de-ionized water. 100 ml of 1N sodium hydroxide and 80 ml of 10% cupric sulphate ($CuSO_4.5H_2O$) are added. 180 g of anhydrous sodium sulphate are dissolved in the mixture, and the volume is brought to 1 liter with de-ionized water.

2. Nelson's color reagent

50 g of ammonium molybdate are dissolved in 900 ml of de-ionized water. Then 42 ml of concentrated sulphuric acid are added, followed by 6 g of disodium hydrogen arsenate heptahydrate dissolved in 50 ml of deionized water, and the volume is brought to 1 litre with deionized water. The solution is allowed to stand for 24-48 hours at 37°C before use and is stored in the dark in a brown glass bottle with a glass stopper.

3. Standard

100 mg of glucose (anhydrous) are dissolved in 1 liter of de-ionized water.

Alternatively, the release of reducing sugars can be measured using a 96 well plate set-up modified after Fox, J.D. & Robyt, J.F. (1991) Anal. Biochem. 195,93-96. Assay conditions are (in brief): 1 ml substrate (e.g. 1% solution) in 50 mM citric acid pH 5 is preincubated at 60°C. A zero timepoint is taken 150 micro l sample and transferred to a microtiter plate well containing 150 micro l solution A + B for reducing sugar determination. The enzymatic reaction is initiated by addition of 100 micro l enzyme and time points are taken at T = 1, 2, 3, 4, and 5 min.

After completion of the assay, the plate is developed by incubation at 85 °C for 70 minutes and the plate is read at 540 nm.

Reagents for determination of reducing value: Solution A) and solution B (62 mg copper sulfate pentahydrate and 63 mg L-serine in 50 ml water).

Pullulanase specificity

Methods for the determination and characterization of the profile of action and specificity of pullulanases for various substrates (e.g., amylopectin, glycogen and pullulan) are described by Kainuma et al. in *Carbohydrate Research,* 61 345-357 (1978). Using these methods, the relative activity of a pullulanase can be determined, and the relative activity of a pullulanase variant according to the invention compared to the relative activity of the parent pullulanase can be assessed, for example to determine whether a pullulanase variant has the desired increased specificity toward high molecular weight saccharides, such as amylopectin, compared to the parent pullulanase.

In order to determine whether the pulluanase variant possesses an increased isoamylase activity as compared to the parent pullulanse the following test may be performed ("assay for isoamylase-like activity"):

1000 mg rabbit liver glycogen is dissolved in 40 ml water to which 0.2% NaOH has been added. 800 mg $NaBH_4$ is added carefully under stirring. The solution is stirred for 48 hours at 25°C after which the reaction is stopped by addition of Amberlite IR-118H (a cation exchanger which removes the boron ions and hence stops the reaction). The solution is filtered to remove the matrix and evaporated to give 10 ml. The solution is then dialyzed extensively against de-ionized water to remove residual boron ions. The parent pullulanase and the pulluanase variant are assayed according to the method of Somogyi-Nelson, using 50 mM sodium acetate, pH values of 4.5, 5.0 or 5.5 and a temperature of 60°C, with a reaction time of 10 minutes. Glucose is used as a standard, a standard curve being made from solutions containing of 0-200 mg glucose/liter.

Clearly, the higher the number of reducing ends formed during the incubation period, the higher "isoamylase activity". The increase in the pullulanase variant's isoamylase activity is expressed as a percentage value based on the original "isoamylase activity" of the parent pullulanase.

Pullulanas variants with altered stability

A variant with improved stability (typically increased thermostability) may be obtained by substitution with proline, substitution of histidine with another amino acid, introduction of a disulfide bond, removal of a deamidation site, altering a hydrogen bond contact, filling in an internal structural cavity with one or more amino acids with bulkier side groups, introduction of interdomain interactions, altering charge distribution, helix capping, or introduction of a salt bridge.

Increased mobility regions:

The following regions have an increased mobility in the crystal structure of Promozyme®, and it is presently believed that these regions can be responsible for stability or activity of the enzyme. Improvements of the enzyme can be obtained by mutation in the below regions and positions. Introducing e.g. larger residues or residues having more atoms in the side chain could increase the stability, or, e.g., introduction of residues having fewer atoms in the side chain could be important for the mobility and thus the activity profile of the enzyme. The regions can be found by analysing the B-factors taken from the coordinate file in Appendix 1, and/or from molecular dynamics calculations of the isotropic fluctuations. These can be obtained by using the program CHARMm from MSI (Molecular simulations inc.).

Thus, in order to stabilize mobile regions in the structure, a preferred variant of a parent pullulanase comprises a modification, e.g., a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1:
408-429 (i.e., 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428 and 429),
300-314 (i.e., 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313 and 314),
157-165 (i.e., 157, 158, 159, 160, 161, 162, 163, 164 and 165),
95-113 (i.e., 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112 and 113),

130-140 (i.e., 130, 131, 132, 133, 134, 135, 136, 137, 138, 139 and 140),
232-238 (i.e., 232, 233, 234, 235,236, 237 and 238),
266-272 (i.e., 266, 267, 268, 269, 270, 271 and 272),
302-308 (i.e., 302, 303, 304, 305, 306, 307 and 308),
418-428 (i.e., 418, 419, 420, 421, 422, 423, 424, 425, 426, 427 and 428),
500-507 (i.e., 500, 501, 502, 503, 504, 505, 506 and 507),
659-665 (i.e., 659, 660, 661, 662, 663, 664 and 665) and
751-755 (i.e., 751, 752, 753, 754 and 755).

Similar modifications, e.g., substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, other preferred modifications, e.g., substitutions, which are believed to stabilized mobile regions in the structure of the pullulanase from *Bacillus deramificans*, correspond to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3:
406-427 (i.e., 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419,
420, 421, 422, 423, 424, 425, 426 and 427),
298-312 (i.e., 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311 and 312),
153-161 (i.e., 153, 154, 155, 156, 157, 158, 159, 160 and 161),
91-109 (i.e., 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108 and 109),
126-136 (i.e., 126, 127, 128, 129, 130, 131, 132, 133, 134, 135 and 136),
230-236 (i.e., 230, 231, 232, 233, 234, 235 and 236),
264-270 (i.e., 264, 265, 266, 267, 268, 269 and 270),
300-306 (i.e., 300, 301, 302, 303, 304, 305 and 306),
416-426 (i.e., 416, 417, 418, 419, 420, 421, 422, 423, 424, 425 and 426),
498-505 (498, 499, 500, 501, 502, 503, 504 and 505),
656-662 (i.e., 656, 657, 658, 659, 660, 661 and 662) and
749-753 (i.e., 749, 750, 751, 752 and 753).

Contemplated combinations of substitutions include according to the invention one or more of: deletion (1-111); deletion(1-113); D562P; G292P; G794P; D148P; N119P; N400S; N400L; N400F; N446S; N446L; N446F; N504S; N504L; N504F; N735S; N735L; N735F; N789S; N789L; N789F; I566A; Q485H; V551I; S492F; D444R; D444K; deletion (154-273).

Multi substitutions of the invention include: deletion(1-111)+D562P; deletion(1-111)+G292P; deletion(1-111)+G794P; deletion(1-111)+D148P; deletion(1-111)+N119P+N400S/L/F; deletion(1-111)+N446L/F; deletion(1-111)+N504S/L/F; deletion(1-111)+N735S/L/F; deletion(1-111)+N789S/L/F; deletion(1-111)+I566A; deletion(1-111)+Q485H; deletion(1-111)+V551I; deletion(1-111)+S492F; eletion(1-111)+D444R/K; eletion(1-111)+deletion(154-273); deletion(1-113)+D562P; deletion(1-111)+G292P; eletion(1-113)+G794P; deletion(1-113)+D148P; deletion(1-113)+N119P+N400S/L/F; deletion(1-131)+N446L/F; eletion(1-113)+N504S/L/F; deletion(1-113)+N735S/L/F; eletion(1-113)+N789S/L/F; deletion(1-113)+I566A; deletion(1-113)+Q485H; deletion(1-113)+V551I; deletion(1-113)+S492F; eletion(1-113)+D444R/K; deletion(1-113)+deletion(154-273); D562P+G292P; D562P+G794P; D562P+D148P; D562P+N119P; D562P+N400S/L/F; D562P+N446S/L/F; D562P+N504S/L/F; D562P+N735S/L/F; D562P+N789S/L/F; D562P+I566A; D562P+Q485H; D562P+V551I; D562P+S492F; D562P+D444R/K; D562P+deletion (154-273); G292P+G794P; G292P+D148P; G292P+N119P; G292P+N400S/L/F; G292P+N446S/L/F; G292P+N504S/L/F; G292P+N735S/L/F; G292P+N789S/L/F; G292P+I566A; G292P+Q485H; G292P+V551I; G292P+S492F; G292P+D444R/K; G292P+deletion (154-273); G794P+D148P; G794P+N119P; G794P+N400S/L/F; G794P+N446S/L/F; G794P+N504S/L/F; G794P+N735S/L/F; G794P +N789S/L/F; G794P+I566A; G794P+Q485H; G794P+V551I; G794P+S492F; G794P+D444R/K; G794P+deletion (154-273); 148P+N119P; D148P+N400S/L/F; D148P+N446S/L/F; D148P+N504S/L/F; D148P+N735S/L/F; D148P+N789S/L/F; D148P+I566A; D148P+Q485H; D148P+V551I; D148P+S492F; D148P+D444R/K; D148P+deletion (154-

273); N119P+N400S/L/F; N119P+N446S/L/F; N119P+N504S/L/F; N119P+N735S/L/F; N119P+N789S/L/F; N119P+I566A; N119P+Q485H; N119P+V551I; N119P+S492F; N119P+D444R/K; N119P+deletion (154-273); N400S/L/F+N446S/L/F; N400S/L/F+N504S/L/F; N400S/L/F+N735S/L/F; N400S/L/F+N789S/L/F; N400S/L/F+I566A; N400S/L/F+Q485H; N400S/L/F+V551I; N400S/L/F+S492F; N400S/L/F+D444R/K; N400S/L/F+deletion (154-273); N446S/L/F+N504S/L/F; N446S/L/F+N735S/L/F; N446S/L/F+N789S/L/F; N446S/L/F+I566A; N446S/L/F+Q485H; N446S/L/F+V551I; N446S/L/F+S492F; N446S/L/F+D444R/K; N446S/L/F+deletion (154-273); N504S/L/F+N735S/L/F; N504S/L/F+N789S/L/F; N504S/L/F+I566A; N504S/L/F+Q485H; N504S/L/F+V551I; N504S/L/F+S492F; N504S/L/F+D444R/K; N504S/L/F+deletion (154-273); N735S/L/F+N789S/L/F; N735S/L/F+I566A; N735S/L/F+Q485H; N735S/L/F+V551I; N735S/L/F+S492F; N735S/L/F+D444R/K; N735S/L/F+deletion (154-273); N789S/L/F+I566A; N789S/L/F+Q485H; N789S/L/F+V551I; N789S/L/F+S492F; N789S/L/F+D444R/K; N789S/L/F+deletion (154-273);I566A+Q485H; I566A+V551I; I566A+S492F; I566A+D444R/K; I566A+deletion (154-273);Q485H+V551I; Q485H+S492F; Q485H+D444R/K; Q485H+deletion (154-273);V551I+S492F; V551I+D444R/K; V551I+deletion (154-273); S492F+D444R/K; S492F+deletion (154-273); D444R/K+deletion (154-273); deletion (1-111)+D562P+N400S/L/F; deletion(1-111)+G292P+N400S/L/F; deletion(1-111)+G794P+N400S/L/F; deletion(1-111)+D148P+N400S/L/F; deletion(1-111)+N119P+N400S/L/F; deletion(1-111)+N446L/F+N400S/L/F; deletion(1-111)+N504S/L/F+N400S/L/F; deletion(1-111)+N735S/L/F+N400S/L/F; deletion(1-111)+N789S/L/F+N400S/L/F; deletion(1-111)+I566A+N400S/L/F; deletion(1-111)+Q485H+N400S/L/F; deletion(1-111)+V551I+N400S/L/F; deletion(1-111)+S492F+N400S/L/F; deletion(1-111)+D444R/K+N400S/L/F; deletion(1-111)+deletion(154-273)+N400S/L/F; deletion(1-111)+D562P; deletion(1-111)+ G292P; eletion(1-111)+G794P; deletion(1-111)+D148P; deletion(1-111)+N119P+N400S/L/F; deletion(1-111)+N446L/F; deletion(1-111)+N504S/L/F; deletion(1-111)+N735S/L/F; deletion(1-

111)+N789S/L/F; deletion(1-111)+I566A; deletion(1-111)+Q485H; deletion(1-111)+V551I;

Furthermore, it is envisaged from the structure that deletion of certain amino acid residues will confer increased stability, such as increased thermostability, to the thus produced variant. Variants, which are believed to be of particular importance, comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

Deletion of the peptide fragment 158-275, such as a deletion starting from position 158, 159, 160 or 161 and ending at position 270, 271, 272, 273, 274 or 275, i.e., the longest deletion will be deletion of the peptide fragment 158-275 and the shortest deletion will be deletion of the peptide fragment 161-270.

Other deletions which are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

Deletion of the peptide fragment 1-315, such as deletion of the peptide fragment 1-314, 1-313, 1-312, 1-311, 1-310, 1-309, 1-308, 1-307, 1-306, 1-305, or 1-304.

Furthermore, the following deletions are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

Deletion of the peptide fragment 1-115, such as deletion of the peptide fragment 1-114, 1-113, 1-112, 1-111, 1-110, 1-109, 1-108, 1-107, 1-106 or 1-105.

Similar deletions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, it is envisaged that deletion of the below amino acid residues will confer increased stability, such as increased thermostability, to the thus produced variant of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3):

Deletion of the peptide fragment 154-273, such as a deletion starting from position 154, 155, 156 or 157 and ending at position 268, 269, 270, 271, 272 or 273, i.e. the longest deletion will be deletion of the peptide fragment 154-273 and the shortest deletion will be deletion of the peptide fragment 157-268.

Other deletions which are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 3:

Deletion of the peptide fragment 1-313, such as deletion of the peptide fragment 1-312, 1-311, 1-310, 1-309, 1-308, 1-307, 1-306, 1-305, 1-304, or 1-303.

Furthermore, the following deletions are expected to confer increased stability, such as increased thermostability, to the pullulanase variant comprises a deletion of amino acid residues corresponding to the following residues of the amino acid sequence set forth in SEQ ID NO: 3:

Deletion of the peptide fragment 1-111, such as deletion of the peptide fragment 1-113, 1-111, 1-110, 1-109, 1-108, 1-107, 1-106, 1-105, 1-104, 1-103, 1-102 or 1-101.

Cavities and crevices

The structure of the pullulanase contains a number of unique internal cavities, which may contain water, and a number of crevices. In order to increase the stability, preferably the thermostability, of the pullulanase it may be desirable to reduce the number or size of cavities and crevices, e.g., by introducing one or more hydrophobic contacts, preferably achieved by introducing amino acids with bulkier side chains in the vicinity or surroundings of the cavity or crevice. For instance, the amino acid residues to be modified are those that are involved in the formation of a cavity or crevice.

In order to determine which amino acid residues of a given enzyme are involved in the formation of cavities or crevices the Conolly program is normally used (B. Lee and F.M. Richards, *J. Mol. Biol.* 55, 379-400 (1971)). The program uses a probe with a certain radius to search the external and internal surface of the protein. The smallest crevice observable in this way has the probe radius.

To analyze the solved structure of Promozyme®, a modified version of the Connolly program included in the program of INSIGHT was used. In the first step, the water molecules and the ions were removed by unmerging these atoms from the solved structure. By using the command MOLECULE SURFACE SOLVENT the solvent accessible surface area was calculated for all atoms and residues using a probe radius of 1.4 Å, and displayed graphically together with the model of the solved structure. The internal cavities are then seen as dot surfaces with no connections to the external surface.

Suggestions for specific modifications to fill out the cavities are given below. By using the homology built structures and/or comparisons based on sequence alignment, mutations for homologous structures of pullulanases can be made.

Accordingly, in a further aspect the present invention relates to a method for constructing a variant of a parent pullulanase, the method comprising:

a) identifying an internal cavity or crevice in the three-dimensional structure of the parent pullulanase;

b) substituting at least one amino acid residue involved in the formation of a cavity or crevice with another amino acid residue which increases the hydrophobic interaction and/or fills out or reduces the size of the cavity or crevice;

c) optionally repeating steps a) and b) recursively;

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);

e) preparing the variant resulting from steps a) - d);

f) testing the stability and/or the temperature dependent activity profile of the variant; and

g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having increased stability and/or an altered temperature dependent activity profile as compared to the parent pullulanase.

In a preferred embodiment of the invention the variant pullanase provided by the above method have increased thermostability as compared to the parent pullulanase. The thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

It will be understood that the cavity or crevice is identified by the amino acid residues surrounding said cavity or crevice, and that modification of said amino acid residues are of importance for filling or reducing the size of the cavity or crevice. Preferably, the modification is a substitution with a bulkier amino acid residue, i.e. one with a greater side chain volume or with an increased number of atoms in the side chain. For example, all the amino acids are bulkier than Gly, whereas Tyr and Trp are bulkier than Phe. The particular amino acid residues referred to below are those that in a crystal structure have been found to flank the cavity or crevice in question.

In a preferred embodiment, the variant of a pullulanase, in order to fill, either completely or partly, cavities or crevices located internally or externally in the structure, comprises a modification, e.g., a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1: 406, 394, 568, 573 576, 563, 557, 396, 392, 515, 583, 442, 792, 767, 732, 760, 783, 740, 688, 478, 534, 550, 627, 314.

In a more preferred embodiment, the variant of a pullulanse comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 1:
G406A, P394F/W/I/L, I568L/F, Y573W, T576N/L/I, S563T, T557N, A396V/L/I, V392, N515M/L/I, V583I/F/L, D442Q, S792Y/F, V767Q/E/L/I, V732I/L, D760Q/E/F/Y, L783F/Y, L740Q,

D688Y/F/E/Q/R/K, L478Q/R, L534F/Y/I, M550F/Y/I/L, L627F/Y/I, L314I.

Similar modifications, e.g., substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, the variant of a pullulanase may also comprise one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:
566, 485, 487, 437, 775, 779, 551, 428, 492, 495, 392, 621, 437+503, 674+664 and 823.

In a more preferred embodiment, the variant of a pullulanse comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:
I566A, Q485H, M487L, D437H, Q775H, E779D, V551I, I428Y/F, S492F, V495I/F/Y, P392Y, L621Q, D437H+D503Y, V674+L664F and L823V.

Disulfide bonds

A variant with improved stability (typically improved thermostability) as compared to the parent pullulanase may be obtained by introducing new interdomain and intradomain contacts, such as establishing inter- or intradomain disulfide bridges.

Accordingly, a further aspect of the present invention relates to a method for constructing a variant of a parent pullulanase, the method comprising:

a) identifying in the three-dimensional structure of the parent pullulanase two or more amino acid residues which, when substituted with cysteines, are capable of forming a disulfide bond;

b) substituting the amino acids identified in a) with cysteines;

c) optionally repeating steps a) and b) recursively;

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);

e) preparing the variant resulting from steps a) - d);

f) testing the stability of said variant; and

g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having increased stability as compared to the parent pullulanase.

In a preferred embodiment of the invention the variant pullanase provided by the above method have increased thermostability as compared to the parent pullulanase. The thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

In order to determine, in the three-dimensional structure of the parent pullulanase, the amino acid residues which, when substituted with cysteines, are capable of forming a disulfide bond, residues with CB atoms less than 4Å from each other, and where the direction of the CA-CB from each residue is pointing towards the other residue are identified. Following the above-mentioned guidelines, the below amino acid residues were identified in the amino acid sequence of SEQ ID NO: 1, and it is contemplated that these residues are suitable for cystein replacement, thereby opening up the possibility of establishing one or more disulfide bridges in the variant pullulanase: K758C+I914C, T916C+A765C, I897C+S819C, P525C+E499C, H286C+T148C.

Similar substitutions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, it is contemplated that the following residues, identified in the amino acid sequence of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3), are suitable for cystein replacement, thereby opening up the possibility of establishing one or more disulfide bridges in the variant pullulanase:

K756C/I912C, M914C/A763C, V895C/G817C, A523C/E497C, H284C/T144C.

Surface charge distribution

A variant with improved stability (typically improved thermostability) as compared to the parent pullulanase may be obtained by changing the surface charge distribution of the pullulanase. For example, when the pH is lowered to about 5 or below histidine residues typically become positively charged and, consequently, unfavorable electrostatic interactions on the protein surface may occur. By engineering the surface charge of the pullulanase one may avoid such unfavorable electrostatic interactions that in turn leads to a higher stability of the pullulanase.

Therefore, a further aspect of the present invention relates to method for constructing a variant of a parent pullulanase, the method comprising:

a) identifying, on the surface of the parent pullulanase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His;

b) substituting, on the surface of the parent pullulanase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His with an uncharged amino acid residue;

c) optionally repeating steps a) and b) recursively;

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);

e) preparing the variant resulting from steps a) - d);

f) testing the stability of said variant; and

g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having increased stability as compared to the parent pullulanase.

As will be understood by the skilled person it may also, in some cases, be advantageous to substitute an uncharged amino acid residue with an amino acid residue bearing a charge or, alternatively, it may in some cases be advantageous to substitute an amino acid residue bearing a charge with an amino

acid residue bearing a charge of opposite sign. Thus, the above-mentioned method may easily be employed by the skilled person also for these purposes. In the case of substituting an uncharged amino acid residue with an amino acid residue bearing a charge the above-mentioned method may be employed the only difference being steps a) and b) which will then read:

a) identifying, on the surface of the parent pullulanase, at least one uncharged amino acid residue;

b) substituting, on the surface of the parent pullulanase, at least one uncharged amino acid residue with a charged amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His.

Also in the case of changing the sign of an amino acid residue present on the surface of the pullulanase the above method may be employed. Again, compared to the above method, the only difference being steps a) and b) which, in this case, read:

a) identifying, on the surface of the parent pullulanase, at least one charged amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His;

b) substituting, on the surface of the parent pullulanase, at least one charged amino acid residue identified in step a) with an amino acid residue having an opposite charge.

Thus, Asp may be substituted with Arg, Lys or His; Glu may be substituted with Arg, Lys or His; Arg may be substituted with Asp or Glu; Lys may be substituted with Asp or Glu; and His may be substituted with Asp or Glu.

In a preferred embodiment of the invention the variant pullulanase provided by the above method(s) have increased thermostability as compared to the parent pullulanase. The thermostability of a given variant may be assessed as described in the above section entitled "Methods for determining stability, activity and specificity".

In order to determine the amino acid residues of a pullulanase, which are present on the surface of the enzyme, the surface accessible area are measured using the DSSP program (Kabsch and Sander, *Biopolymers* (1983), 22, 2577-2637). All

residues having a surface accessibilty higher than 0 is regarded a surface residue.

The amino acid residues found on the surface of Promozyme® using the above method are as follows:

E526, Q544, E760, N338, N228, N181,

and it is contemplated that the following substitutions are of particular interest:

E526H, Q544E, E760Q, N338K/R, N228DE/, N181K/R.

Similar substitutions may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, the variant of a pullulanase may also comprise one or more modifications, e.g., substitutions, corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:

444, 530, 710 and 855.

In a more preferred embodiment, the variant of a pullulanse comprises one or more substitutions corresponding to the following substitutions in the amino acid sequence set forth in SEQ ID NO: 3:

D444R/K, K530Y/F/L, N710R and T855K.

Other modifications

Variants with improved stability, in particular variants with improved thermostability, can be obtained by improving existing or introducing new interdomain or intradomain contacts. Such improved stability can be achieved by the modifications listed below.

Thus, one preferred embodiment of the invention relates to a variant of a parent pullulanase which has an improved stability and one or more salt bridges as compared to the parent pullulanase, wherein said variant comprises a modifications, e.g., a substitution, in a position corresponding to at least one of the following sets of positions in SEQ ID NO: 1:

301, 385, 298, 299, 385 and 299+385, in particular L301R, N385R, H298R, N299R, N385D and N299R+N385D.

Similar modifications, e.g., substitutions, may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

For example, it is contemplated that the following substitutions in the pullunanase having the amino acid sequence set forth in SEQ ID NO: 3 will enhance the stability of the enzyme: T891D, S892K, T891D+S892K and N400R.

In another preferred embodiment, the variant of the pullulanase comprises a substitution corresponding to one or more of the following substitutions with proline in the amino acid sequence set forth in SEQ ID NO: 1:

G293P, K151P, K122P, N315P, N374P, N793P, A446P, G672P, G668P, T556P

In a further interesting embodiment of the invention, the variant of the pullulanase comprises a substitution corresponding to one or more of the following substitutions with proline in the amino acid sequence set forth in SEQ ID NO: 3:

D562P, G794P, G292P, D148P, N119P, D314P, N373P, N792P, G671P, G667P, and T554P.

Analogously, it may be preferred that one or more histidine residue(s) present in the parent pullulanase is (are) substituted with a non-histidine residues such as Y, V I, L, F, M, E, Q, N, or D. Accordingly, in another preferred embodiment, the variant of the parent pullulanase comprises a substitution of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3: H422Y/F/L, H483Y/F/L, H543Y/F/L/N and H613Y/F/L.

It may be preferred that one or more asparagine or glutamine residues present in the parent pullulanase is or are substituted with a residue lacking the amide group on the side chain. Preferably, such asparagines or glutamine residues are substituted with S, T, V, L and/or F amino acid residues. Accordingly, in another preferred embodiment, the variant of the parent pullulanase comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or

more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1:

Q543, Q339, N337, Q380, Q353, N384, N286, N298, N227, Q227, Q210, N180, Q259, N583, N790, N793, N505, N788, N736, N684, N689 or N681, preferably Q543S/T/V/L/F, Q339S/T/V/L/F, N337S/T/V/L/F, Q380S/T/V/L/F, Q353S/T/V/L/F, N384S/T/V/L/F, N286S/T/V/L/F, N298S/T/V/L/F, N227S/T/V/L/F, Q227S/T/V/L/F, Q210S/T/V/L/F, N180S/T/V/L/F, Q259S/T/V/L/F, N583S/T/V/L/F, N790S/T/V/L/F, N793S/T/V/L/F, N505S/T/V/L/F, N788S/T/V/L/F, N736S/T/V/L/F, N684S/T/V/L/F, N689S/T/V/L/F and N681S/T/V/L/F.

The corresponding residues found in the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) include:

N400, N446, N504, N717, N735 and N789, preferably N400S/T/V/L/F, N446S/T/V/L/F, N504S/T/V/L/F, N717S/T/V/L/F, N735S/T/V/L/F, and N789S/T/V/L/F.

Moreover, it is contemplated that modifications, e.g. substitutions, in the region linking the N2 and the A domain, as well as other regions linking other domains, will confer additional stability, such as an increased thermostability, to the enzyme. Thus, in an interesting embodiment of the invention, the pullulanase variant comprises one or more modifications, e.g., substitutions, in the domain-linking regions (e.g., the region linking the N2 and A domains).

Examples of such modifications include one or more of the following substitutions in the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3):

111, 112,
158-160 (i.e., 158, 159 and 160),
270-274 (i.e., 270, 271, 272, 273 and 274),
302-314 (i.e., 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313 and 314) and
408-426 (i.e., 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425 and 426).

Examples of specific substitutions are: S111T/V/L, N112S/T/Q, S158Y/F/T, L159Y/K/R/A/S/T, G160A/S/T, D270E/S/T, L271V/I, V272I, T273N/D/E/Y/F, V274I, N302V/L/Y, N305V/L/Y, S306T/V, Q308K/R/A/S/T, Y309F, Y310E/D/Q/N/L/V/I, D314A/S/T, L409N, D408S/T, A410S/T, D413R/K/S/T, A415S/T, G416S/T/V,

N418A/V/S/T, S419D/N/T, K421E/Q/S/T/V/A, H422D/L/Y/F, I423L/V/S/T/N/Q, T424S/A and K426A/S/T.

Other substitutions that are considered of particular importance in SEQ ID NO: 3 include D437N and D440N.

Similar modifications, e.g., substitutions, may be introduced in equivalent positions of other pullulanases. Modifications of particular interest are any combination of one or more of the above with any of the other modifications disclosed herein.

Before actually constructing a pullulanase variant to achieve any of the above objectives, it may be convenient to evaluate whether or not the contemplated amino acid modification can be accommodated into pullulanase structure, e.g., in a model of the three-dimensional structure of the parent pullulanase.

Pullulanase variants with altered substrate specificity

One aim of the present invention is to change the degradation characteristics of a pullulanase. Thus, as Promozyme® (and pullulanases in general) exhibits a low activity towards high molecular weight branched starchy material, such as glycogen and amylopectin, it may be desirable to change this cleavage pattern, e.g., so as to obtain a higher activity against such substrates, in particular when the pullulanase is to be added during the liquefaction process.

An altered substrate specificity may be achieved by modifying the substrate binding area in a parent pullulanse.

Accordingly, the present invention also relates to a method for constructing a variant of a parent pullulanase, the method comprising:

a) identifying the substrate binding area in a model of the three-dimensional structure of the parent pullulanase;

b) modifying the substrate binding area by an amino acid substitution, deletion and/or insertion;

c) optionally repeating step b) recursively;

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),

e) preparing the variant resulting from steps a) - d);

f) testing the substrate specificity of the variant;

g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having an altered substrate specificity as compared to the parent pullulanase.

The substrate binding area may easily be identified by homology to other family 13 members. The active site residues are identified by homology. The substrate-binding site is identified by the concave cavity containing the active site residues. A substrate model is docked into the cavity. A suitable substrate model is the substrate structure found in the pdb file 1BAG termed GLC. This model can be "docked" into the Promozyme X-ray structure or a modeled Pullulanase 3D structure by superimposing the active site residues in the two structures. In 1BAG one of the active site residues has been mutated into a Gln instead of the native Glu. The active site residues to be superimposed are: D269, Q208 and D176 (1BAG) with D736, E651 and D622 (Promozyme®). The superposition can be made using the program INSIGHTII.

Without being limited to any theory, it is presently believed that binding between a substrate and an enzyme is supported by favorable interactions found within a sphere 10 Å from the substrate molecule, in particular within a sphere of 6 Å from the substrate molecule. Examples of such favorable bonds are hydrogen bonds, strong electrostatic interaction and/or hydrophobic interactions. The following residues of Promozyme® (SEQ ID NO: 1), are within a distance of 10 Å from the "docked" substrate and thus believed to be involved in interactions with said substrate:

437, 439, 487, 489, 490, 514, 679, 681, 684, 685, 731, 775, 786,

494-496 (i.e., 494, 495 and 496),

505-511 (i.e., 505, 506, 507, 508, 509, 510 and 511),

551-559 (i.e., 551, 552, 553, 554, 555, 556, 557, 558 and 559),

584-590 (i.e., 584, 585, 586, 587, 588, 589 and 590),

620-626 (i.e., 620, 621, 622, 623, 624, 625, 626),

650-658 (i.e., 659, 651, 652, 653, 654, 655, 656, 657 and 658),

665-668 (i.e., 666, 667 and 668),

690-693 (i.e., 690, 691, 692 and 693),
734-738 (i.e., 734, 735, 736, 737 and 738) and
789-795 (i.e., 789, 790, 791, 792, 793, 794 and 795).

The following residues of Promozyme® are within a distance of 6 Å from the substrate and thus believed to be involved in interactions with said substrate:
489, 551, 553, 555, 556, 620, 651, 691, 692, 791, 793, 794,
506-510 (i.e., 507, 508, 509 and 510),
586-588 (i.e., 586, 587 and 588),
622-624 (i.e., 622, 623 and 624),
653-656 (i.e., 653, 654, 655 and 656) and
735-737 (i.e., 735, 736 and 737),

In a preferred embodiment of the invention, the parent pullulanase is modified in such a way that the variant pulluanase exhibits an increased isoamylase activity compared to the parent pullulanase.

When used herein, the term "increased isoamylase activity" refers in general to the fact that the pullulanase variants according to the invention exhibits a higher activity towards high molecular weight branched starchy material, such as glycogen and amylopectin as compared to the parent pullulanase, cf. above.

In an interesting embodiment of the invention the pullulanase variant has an increased isoamylase activity as defined by an increase of at least 5%, preferably of at least 10%, more preferably of at least 15%, more preferably of at least 25%, most preferably of at least 50%, in particular of at least 75%, such as of at least 100% in the number of reducing ends formed in the "assay for isoamylase-like activity" described herein, using 50 mM sodium acetate, a pH of 4.5, 5.0 or 5.5, a temperature of 60°C and when incubated with a 10 w/v rabbit liver glycogen solution for a period of 10 min.

Similar modifications may be introduced in equivalent positions of other pullulanases. Substitutions of particular interest are any combination of one or both of the above with any of the other modifications disclosed herein.

For example, the following residues of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) are within a distance

of 10 Å from the "docked" substrate and thus believed to be involved in interactions with said substrate:

435, 437, 485, 487, 488, 512, 677, 679, 682, 683, 729, 773, 784,

492-494 (i.e., 492, 493 and 494),

503-509 (i.e., 503, 504, 505, 506, 507, 508 and 509),

549-557 (i.e., 549, 550, 551, 552, 553, 554, 555, 556 and 557),

582-588 (i.e., 582, 583, 584, 585, 586, 587 and 588),

618-624 (i.e., 618, 619, 620, 621, 622, 623 and 624),

648-656 (i.e., 648, 649, 650, 651, 652, 653, 654, 655 and 656),

663-666 (i.e., 663, 664, 665 and 666),

688-691 (i.e., 688, 689, 690 and 691),

732-736 (i.e., 732, 733, 734, 735 and 736) and

787-793 (i.e., 787, 788, 879, 790, 791, 792 and 793).

The following residues of the pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) are within a distance of 6 Å from the substrate and thus believed to be involved in interactions with said substrate:

487, 549, 551, 553, 554, 618, 649, 689, 690, 789, 791, 792,

504-508 (i.e., 504, 505, 506, 507 and 508),

584-586 (i.e., 584, 585 and 586),

620-622 (i.e., 620, 621 and 622),

651-654 (i.e., 651, 652, 653 and 654) and

733-735 (i.e., 733, 734 and 735).

Examples of specific modifications in the above-mentioned regions of *Bacillus deramificans* are: L621I/V, D508M/N/L/T/V, T586I/L/V, T677W/F/Y, Y729F/I/L, D679G/A/V, S732V/T/L/I, N735G/L/V/I/S/T/A and Δ(688-691).

Pullulanase variants with altered pH dependent activity profile

The pH dependent activity profile can be changed by changing the pKa of residues within 15 Å, in particular by changing the pKa of residues within 10 Å, from the active site residues of the parent pullulanase. Changing the pKa of the active site residues is achieved, e.g., by changing the electrostatic interaction or hydrophobic interaction between functional groups of amino acid side chains of a given amino acid residue and its close surroundings. To obtain a higher

activity at a higher pH, negatively charged residues are placed near a hydrogen donor acid, whereas positively charged residues placed near a nucleophilic acid will result in higher activity at low pH. Also, a decrease in the pKa can be obtained by reducing the accessibility of water or increasing hydrophobicity of the environment.

It is preferred that the variant in question exhibits a pH optimum which is at least about 0.5 pH units higher or lower, preferably at least about 1.0 pH units higher or lower, than the corresponding pH optimum of the parent pullulanase when tested on a suitable substrate (e.g. pullulan, amylopectin or glycogen).

Furthermore, it is particular preferred that the variant in question exhibits an increased activity in the pH range of from 4 to 5.5 as compared to the parent pullulanase when tested on a suitable substrate (e.g., pullulan, amylopectin or glycogen).

Thus, another aspect of the present invention relates to a method for constructing a variant of a parent pullulanase, the method comprising:

a) identifying an amino acid residue which is within 15 Å, in particular within 10 Å, from an active site residue of the parent pullulanase in the three-dimensional structure of said parent pullulanse, and which is involved in electrostatic or hydrophobic interactions with an active site residue;

b) substituting said amino acid residue with another amino acid residue which changes the electrostatic and/or hydrophobic surroundings of an active site residue, and which can be accommodated in the structure;

c) optionally repeating steps a) and b) recursively;

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);

e) preparing the variant resulting from steps a) - d);

f) testing the pH dependent activity of said variant; and

g) optionally repeating steps a) - f) recursively; and

h) selecting a variant having an altered pH dependent activity as compared to the parent amylase.

In general, an amino acid residue which is within 15 Å or 10Å, respectively, from an active site residue of the parent pullulanase may be identified by using the INSIGHTII program.

In a preferred embodiment, the variant of a parent pullulanase having an altered pH dependent activity profile as compared to the parent pullulanase comprises a modification, e.g. a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 1 (all within 15Å from the active site residues D736, E651, D622):
430, 433, 518, 521, 565, 599, 600, 610, 611, 635, 636, 639, 717, 760, 763, 764, 767, 817,
435-443 (i.e., 435, 436, 437, 438, 439, 440, 441, 442, and 443),
486-496 (i.e., 486, 487, 488, 489, 490, 491, 492, 493, 494, 495 and 496),
505-515 (i.e., 505, 506, 507, 508, 509, 510, 511, 512, 513, 514 and 515),
548-560 (i.e., 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559 and 560),
573-575, (i.e., 573, 574 and 575),
583-595 (i.e., 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594 and 594),
602-604 (i.e., 602, 603 and 604),
606-608 (i.e., 606-607 and 608),
616-633 (i.e., 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, and 633),
646-672 (i.e., 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671 and 672),
674-696 (i.e., 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695 and 696), 720-722 (i.e. 720, 721 and 722),
725-747 (i.e., 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746 and 747), 773-781 (i.e. 773, 774, 775, 776, 777, 778, 779, 780 and 781), 783-797 (i.e. 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796 and 797). and

799-802 (i.e., 799, 800, 801 and 802).

Within 10Å from the active site residues D736, E651, D622:

437, 442, 492, 514, 575, 594, 603, 632, 635, 684, 688, 691, 692, 721, 727, 729, 742, 743, 775, 777, 778, 780, 784, 786, 800,

487-490 (i.e., 487, 488, 489 and 490),

507-511 (i.e., 507, 508, 509, 510 and 511),

550-557 (i.e., 550, 551, 552, 553, 554, 555, 556 and 556),

585-588 (i.e., 585, 586, 587 and 588),

590-592 (i.e., 590, 591 and 592),

619-628 (i.e., 619, 620, 621, 622, 623, 624, 625, 626, 627 and 628), 648-655 (i.e., 648, 649, 650, 651, 652, 653, 654 and 655),

665-671 (i.e., 665, 666, 667, 668, 669, 670 and 671),

676-681 (i.e., 676, 677, 678, 679, 680 and 681),

731-740 (i.e., 731, 732, 733, 734, 735, 736, 737, 738, 739 and 740) and

788-793 (i.e., 788, 789, 790, 791, 792 and 793).

Similar modifications may be introduced in equivalent positions of other pullulanases. Variants of particular interest have a combination of one or more of the above with any of the other modifications disclosed herein.

Thus, in another preferred embodiment, the variant of a parent pullulanase having an altered pH dependent activity profile as compared to the parent pullulanase comprises a modification, e.g., a substitution, of an amino acid residue corresponding to one or more of the following residues of the amino acid sequence set forth in SEQ ID NO: 3 (all within 15 Å from the active site residues D734, E649 and D620):

428, 431, 516, 519, 563, 597, 598, 608, 609, 633, 634, 637, 715, 758, 761, 762, 765, 815,

433-441 (i.e., 433, 434, 435, 436, 437, 438, 439, 440 and 441),

484-494 (i.e., 484, 485, 486, 487, 488, 489, 490, 491, 492, 493 and 494),

503-513 (i.e., 503, 504, 505, 506, 507, 508, 509, 510, 511, 512 and 513),

546-558 (546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557 and 558),
571-573 (i.e., 571, 572 and 573),
581-593 (i.e., 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592 and 593),
600-602 (i.e., 600, 601 and 602),
604-606 (i.e., 604, 605 and 606),
614-631 (i.e., 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630 and 631),
644-670 (i.e., 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669 and 670),
672-694 (i.e., 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690,691, 692, 693 and 694),
718-720 (i.e., 718, 719 and 720),
723-745 (i.e., 723, 734, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744 and 745),
771-779 (i.e., 771, 772, 773, 774, 775, 776, 777, 778 and 779),
781-795 (i.e. 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794 and 795) and
797-800 (i.e., 797, 798, 799 and 800).

Within 10 Å from the active site residues D734, E649 and D620:
435, 440, 490, 512, 573, 601, 605, 630, 669, 682, 686, 689, 690, 719, 725, 727, 740, 741, 773, 775, 776, 778, 782, 784, 798,
485-488 (i.e., 485, 486, 487 and 488),
505-509 (i.e., 505, 506, 507, 508 and 509),
548-555 (i.e., 548, 549, 550, 551, 552, 553, 554 and 555),
583-586 (i.e., 583, 584, 585 and 586),
588-590 (i.e., 588, 589 and 590),
617-626 (i.e., 616, 617, 618, 619, 620, 621, 622, 623, 624, 625 and 626),
646-653 (i.e., 646, 647, 648, 649, 650, 651, 652 and 653),
663-667 (i.e., 663, 664, 665, 666 and 667),
674-679 (i.e., 674, 675, 676, 677, 678 and 679),

729-738 (i.e., 729, 730, 731, 732, 733, 734, 735, 736, 737 and 738) and

786-791 (i.e., 786, 787, 788, 789, 790 and 791).

Specific examples of substitutions in the above-mentioned positions include D437L/I/V/F, D440L/I/V/F, M486K, M487K, D503L/I/V/F, D508N/L/T/V, T586V/I, M630H and D437L/I/V/F+D440L/I/V/F+D503L/I/V/F.

Nomenclature for amino acid modifications

The nomenclature used herein for defining modifications is essentially as described in WO 92/05249. Thus, G406A indicates a substitution of the amino acid G (Gly) in position 406 with the amino acid A (Ala). G406 indicates a substitution of the amino acid G (Gly) with any other amino acid. P394F/W/I/L or P394F,W,I,L indicates a substitution of P394 with F, W, I or L. Δ(688-691) indicates a deletion of amino acids in positions 688-691. 412-A-413 indicates an insertion of A between amino acids 412 and 413.

A deletion of Alanine in position A30 is shown as:

A30*

and insertion of an additional amino acid residue, such as Lysine, is shown as:

A30AK

Where a specific pullulanase contains a "deletion" in comparison with other pullulanases and an insertion is made in such a position this is indicated as:

*36D

for insertion of an Aspartic acid in position 36.

Multiple mutations are separated by plus signs, i.e.:

A30N+E34S or A30N/E34S

representing mutations in positions 30 and 34 substituting Alanine and Glutamic acid for Asparagine and Serine, respectively.

Furthermore, when a position suitable for modification is identified herein without any specific modification being suggested, it is to be understood that any amino acid residue may be substituted for the amino acid residue present in the position. Thus, for instance, when a modification of an alanine

in position 30 is mentioned, but not specified, it is to be understood that the Alanine may be deleted or substituted for any other amino acid, i.e., any one of: R,N,D,A,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V.

Further, "A30X" means any one of the following substitutions: A30R, A30N, A30D, A30C, A30Q, A30E, A30G, A30H, A30I, A30L, A30K, A30M, A30F, A30P, A30S, A30T, A30W, A30Y, or A30 V; or in short: A30R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V.

When used herein, the term "modification" (of a particular amino acid residue) is intended to cover substitution and deletion (of the particular amino acid residue) as well as insertion of one or more amino acid residues after the particular amino acid residue.

Polypeptide sequence homology

For purposes of the present invention, the degree of homology may be suitably determined according to the method described in S.B. Needleman and C.D. Wunsch, *Journal of Molecular Biology*, 48, 443-45, with the following settings for polypeptide sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1. The determination may be done by means of a computer program known such as GAP provided in the UWGCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711).

Hybridization

Suitable experimental conditions for determining hybridization between a nucleotide probe and a homologous DNA or RNA sequence involves presoaking of the filter containing the DNA fragments or RNA to hybridize in 5x SSC (sodium chloride/sodium citrate, Sambrook, et al. Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989) for 10 min, and prehybridization of the filter in a solution of 5x SSC, 5x Denhardt's solution (Sambrook, et al., 1989), 0.5% SDS and 100 micro g/ml of denatured sonicated salmon sperm DNA (Sambrook, et al., 1989), followed by hybridization in the same

solution containing a random-primed (A. P. Feinberg B. and Vogelstein, *Anal. Biochem.* 132, 6-13 (1983)), ^{32}P-dCTP-labeled (specific activity > 1 x 10^9 cpm/micro g) probe for 12 hours at ca. 45°C. The filter is then washed twice for 30 minutes in 2x SSC, 0.5% SDS at least 55°C (low stringency), preferably at least 60°C (medium stringency), more preferably at least 65°C (medium/high stringency), more preferably at least 70°C (high stringency), even more preferably at least 75°C (very high stringency).

Molecules which hybridize to the oligonucleotide probe under these conditions are detected by exposure to x-ray film.

Methods of preparing pullulanase variants according to the invention

<u>Cloning a DNA sequence encoding a pullulanase</u>

The DNA sequence encoding a parent pullulanase may be isolated from any cell or microorganism producing the pullulanase in question, using various methods well known in the art.

First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the pullulanase to be studied. Then, if the amino acid sequence of the pullulanase is known, homologous, labelled oligonucleotide probes may be synthesised and used to identify pullulanase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labelled oligonucleotide probe containing sequences homologous to a known pullulanase gene could be used as a probe to identify pullulanase-encoding clones, using hybridization and washing conditions of lower stringency.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, e.g. the phosphoroamidite method described by S.L. Beaucage and M.H. Caruthers, *Tetrahedron Letters*, 22, 1859-1869 (1981) or the method described by Matthes et al. *The EMBO*, 3, 801-805 (1984). In the phosphoroamidite method, oligonucleotides are syn-

thesized, e.g., in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating fragments of synthetic, genomic or cDNA origin, wherein the fragments correspond to various parts of the entire DNA sequence, in accordance with techniques well known in the art. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al. *Science*, 239, 487-491(1988).

Site-directed Mutagenesis

Once a pullulanase-encoding DNA sequence has been isolated, and desirable sites for modification identified, modifications may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired modification sites; mutant nucleotides are inserted during oligonucleotide synthesis. In a specific method, a single-stranded gap of DNA, bridging the pullulanase-encoding sequence, is created in a vector carrying the pullulanase gene. Then the synthetic nucleotide, bearing the desired modification, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is then filled in with DNA polymerase I (Klenow fragment) and the construct is ligated using T4 ligase. A specific example of this method is described in Morinaga et al. *Biotechnology* 2, 639-646 (1984). US 4,760,025 disclose the introduction of oligonucleotides encoding multiple modifications by performing minor alterations of the cassette. However, an even greater variety of modifications can be introduced at any one time by the Morinaga method because a multitude of oligonucleotides, of various lengths, can be introduced.

Another method of introducing modifications into a pullulanase-encoding DNA sequences is described in Nelson and Long *Analytical Biochemistry*, 180, 147-151 (1989). It involves a 3-step generation of a PCR fragment containing the desired modification introduced by using a chemically synthesized DNA

strand as one of the primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the modification may be isolated by cleavage with restriction endonucleases and reinserted into an expression plasmid.

Random Mutagenesis

Random mutagenesis is suitably performed either as localized or region-specific random mutagenesis in at least three parts of the gene translating to the amino acid sequence shown in question, or within the whole gene.

The random mutagenesis of a DNA sequence encoding a parent pullulanase may be conveniently performed by use of any method known in the art.

In relation to the above, a further aspect of the present invention relates to a method for generating a variant of a parent pullulanase, wherein the variant exhibits an altered property, such as increased thermostability, increased stability at low pH and at low calcium concentration, relative to the parent pullulanase, the method comprising:

(a) subjecting a DNA sequence encoding the parent pullulanase to random mutagenesis,

(b) expressing the mutated DNA sequence obtained in step (a) in a host cell, and

(c) screening for host cells expressing a pullulanase variant which has an altered property relative to the parent pullulanase.

Step (a) of the above method of the invention is preferably performed using doped primers.

For instance, the random mutagenesis may be performed by use of a suitable physical or chemical mutagenizing agent, by use of a suitable oligonucleotide, or by subjecting the DNA sequence to PCR generated mutagenesis. Furthermore, the random mutagenesis may be performed by use of any combination of these mutagenizing agents. The mutagenizing agent may, e.g., be one which induces transitions, transversions, inversions, scrambling, deletions, and/or insertions.

Examples of a physical or chemical mutagenizing agent suitable for the present purpose include ultraviolet (UV) ir-

radiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine (MNNG), O-methyl hydroxylamine, nitrous acid, ethyl methane sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide analogues. When such agents are used, the mutagenesis is typically performed by incubating the DNA sequence encoding the parent enzyme to be mutagenized in the presence of the mutagenizing agent of choice under suitable conditions for the mutagenesis to take place, and selecting for mutated DNA having the desired properties.

When the mutagenesis is performed by the use of an oligonucleotide, the oligonucleotide may be doped or spiked with the three non-parent nucleotides during the synthesis of the oligonucleotide at the positions that are to be changed. The doping or spiking may be done so that codons for unwanted amino acids are avoided. The doped or spiked oligonucleotide can be incorporated into the DNA encoding the pullulaase enzyme by any published technique, using, e.g., PCR, LCR or any DNA polymerase and ligase as deemed appropriate.

Preferably, the doping is carried out using "constant random doping", in which the percentage of wild-type and modification in each position is predefined. Furthermore, the doping may be directed toward a preference for the introduction of certain nucleotides, and thereby a preference for the introduction of one or more specific amino acid residues. The doping may be made, e.g., so as to allow for the introduction of 90% wild type and 10% modifications in each position. An additional consideration in the choice of a doping scheme is based on genetic as well as protein-structural constraints. The doping scheme may be made by using the DOPE program which, *inter alia*, ensures that introduction of stop codons is avoided (L.J. Jensen et al. *Nucleic Acid Research*, 26, 697-702 (1998).

When PCR-generated mutagenesis is used, either a chemically treated or non-treated gene encoding a parent pullulanase enzyme is subjected to PCR under conditions that increase the misincorporation of nucleotides (Deshler 1992; Leung et al., *Technique*, 1, 1989, pp. 11-15).

A mutator strain of *E. coli* (Fowler et al., *Molec. Gen. Genet.*, 133, 1974, 179-191), *S. cereviseae* or any other

microbial organism may be used for the random mutagenesis of the DNA encoding the pullulanase by, e.g., transforming a plasmid containing the parent enzyme into the mutator strain, growing the mutator strain with the plasmid and isolating the mutated plasmid from the mutator strain. The mutated plasmid may be subsequently transformed into the expression organism.

The DNA sequence to be mutagenized may conveniently be present in a genomic or cDNA library prepared from an organism expressing the parent pullulanase. Alternatively, the DNA sequence may be present on a suitable vector such as a plasmid or a bacteriophage, which as such may be incubated with or otherwise exposed to the mutagenising agent. The DNA to be mutagenized may also be present in a host cell either by being integrated in the genome of said cell or by being present on a vector harbored in the cell. Finally, the DNA to be mutagenized may be in isolated form. It will be understood that the DNA sequence to be subjected to random mutagenesis is preferably a cDNA or a genomic DNA sequence.

In some cases it may be convenient to amplify the mutated DNA sequence prior to performing the expression step b) or the screening step c). Such amplification may be performed in accordance with methods known in the art, the presently preferred method being PCR-generated amplification using oligonucleotide primers prepared on the basis of the DNA or amino acid sequence of the parent enzyme.

Subsequent to the incubation with or exposure to the mutagenising agent, the mutated DNA is expressed by culturing a suitable host cell carrying the DNA sequence under conditions allowing expression to take place. The host cell used for this purpose may be one which has been transformed with the mutated DNA sequence, optionally present on a vector, or one which was carried the DNA sequence encoding the parent enzyme during the mutagenesis treatment. Examples of suitable host cells are the following: gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*,

Streptomyces lividans or *Streptomyces murinus*; and gram negative bacteria such as *E. coli*.

The mutated DNA sequence may further comprise a DNA sequence encoding functions permitting expression of the mutated DNA sequence.

Localized random mutagenesis

The random mutagenesis may be advantageously localized to a part of the parent pullulanase in question. This may, e.g., be advantageous when certain regions of the enzyme have been identified to be of particular importance for a given property of the enzyme, and when modified are expected to result in a variant having improved properties. Such regions may normally be identified when the tertiary structure of the parent enzyme has been elucidated and related to the function of the enzyme.

The localized, or region-specific, random mutagenesis is conveniently performed by use of PCR generated mutagenesis techniques as described above or any other suitable technique known in the art. Alternatively, the DNA sequence encoding the part of the DNA sequence to be modified may be isolated, e.g., by insertion into a suitable vector, and said part may be subsequently subjected to mutagenesis by use of any of the mutagenesis methods discussed above.

General method for random mutagenesis by use of the DOPE program

The random mutagenesis may be carried out by the following steps:

1. Select regions of interest for modification in the parent enzyme
2. Decide on mutation sites and non-mutated sites in the selected region
3. Decide on which kind of mutations should be carried out, e.g. with respect to the desired stability and/or performance of the variant to be constructed
4. Select structurally reasonable mutations
5. Adjust the residues selected by step 3 with regard to step 4.

6. Analyze by use of a suitable dope algorithm the nucleotide distribution.

7. If necessary, adjust the wanted residues to genetic code realism, e.g. taking into account constraints resulting from the genetic code, e.g. in order to avoid introduction of stop codons; the skilled person will be aware that some codon combinations cannot be used in practice and will need to be adapted

8. Make primers

9. Perform random mutagenesis by use of the primers

10. Select resulting pullulanase variants by screening for the desired improved properties.

Suitable dope algorithms for use in step 6 are well known in the art. One such algorithm is described by Tomandl, D. et al., 1997, Journal of Computer-Aided Molecular Design 11:29-38. Another algorithm is DOPE (Jensen, LJ, Andersen, KV, Svendsen, A, and Kretzschmar, T (1998) Nucleic Acids Research 26:697-702).

Expression of pullulanase variants

The construction of the variant of interest is accomplished by cultivating a microorganism comprising a DNA sequence encoding the variant under conditions which are conducive for producing the variant, and optionally subsequently recovering the variant from the resulting culture broth. This is described in detail further below.

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in the form of a protein or polypeptide, using an expression vector which typically includes control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

The recombinant expression vector carrying the DNA sequence encoding an pullulanase variant of the invention may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the

vector may be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an artificial chromosome. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence that shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding a pullulanase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dag*A promoters, the promoters of the *Bacillus licheniformis* α-amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* alpha-amylase (*amyQ*), the promoters of the *Bacillus subtilis* xylA and xylB genes, etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral alpha-amylase, *A. niger* acid stable alpha-amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase (TPI) or *A. nidulans* acetamidase.

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the pullulanase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples

of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as amdS, argB, niaD and sC, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, e.g., as described in WO 91/17243.

While intracellular expression may be advantageous in some respects, e.g., when using certain bacteria as host cells, it is generally preferred that the expression is extracellular. In general, the *Bacillus* α-amylases mentioned herein comprise a preregion permitting secretion of the expressed protease into the culture medium. If desirable, this preregion may be replaced by a different preregion or signal sequence, conveniently accomplished by substitution of the DNA sequences encoding the respective preregions.

The procedures used to ligate the DNA construct of the invention encoding the pullulanase variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al. Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989).

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of a pullulanase variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromo-

some may be performed according to conventional methods, e.g. by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g., a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, or *Streptomyces lividans* or *Streptomyces murinus*, or gram negative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

The yeast organism may favourably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, e.g. *Saccharomyces cerevisiae*. The filamentous fungus may advantageously belong to a species of *Aspergillus*, e.g. *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known *per se*. A suitable procedure for transformation of *Aspergillus* host cells is described in EP 238 023.

In a yet further aspect, the present invention relates to a method for producing a pullulanase variant of the invention, the method comprising: cultivating a host cell as described above under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the pullulanase variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes

(e.g., as described in catalogues of the American Type Culture Collection).

The pullulanase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulfate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

Testing of pullulanase

Pullulanase variants produced by any of the methods described above may be tested, either prior to or after purification, for pullulanase activity in a screening assay which measures the ability of the variant to degrade pullulan or, in case it is desired to screen for an increased isoamylases activity, the ability of the variant to degrade amylopectin. The screening in step 10 in the above-mentioned random mutagenesis method of the invention may be conveniently performed by use of a filter assay based on the following procedure: A microorganism capable of expressing the mutated pullulanase of interest is incubated on a suitable medium and under suitable conditions for secretion of the enzyme, the medium being covered with two filters comprising a protein-binding filter placed under a second filter exhibiting a low protein binding capability. The microorganism is grown on the second, top filter. Subsequent to the incubation, the bottom protein-binding filter comprising enzymes secreted from the microorganism is separated from the second filter comprising the microorganism. The protein-binding filter is then subjected to screening for the desired enzymatic activity, and the corresponding microbial colonies present on the second filter are identified. The first filter used for binding the enzymatic activity may be any protein-binding filter, e.g., nylon or nitrocellulose. The second filter carrying the colonies of the expression organism may be any filter that has no or low

affinity for binding proteins, e.g., cellulose acetate or DURAPORA™.

Screening consists of treating the first filter to which the secreted protein is bound with a substrate that allows detection of the activity. The enzymatic activity may be detected by a dye, fluorescence, precipitation, pH indicator, IR-absorbance or any other known technique for detection of enzymatic activity. The detecting compound may be immobilized by any immobilizing agent, e.g., agarose, agar, gelatine, polyacrylamide, starch, filter paper, cloth; or any combination of immobilizing agents. For example, isoamylase activity can be detected by Cibacron Red labelled amylopectin, which is immobilized in agarose. isoamylase activity on this substrate produces zones on the plate with reduced red color intensity (clearing zones).

To screen for variants with increased stability, the filter with bound pullulanase variants can be pretreated prior to the detection step described above to inactivate variants that do not have improved stability relative to the parent pullulanase. This inactivation step may consist of, but is not limited to, incubation at elevated temperatures in the presence of a buffered solution at any pH from pH 2 to 12, and/or in a buffer containing another compound known or thought to contribute to altered stability, e.g., surfactants, EDTA, EGTA, wheat flour components, or any other relevant additives. Filters so treated for a specified time are then rinsed briefly in deionized water and placed on plates for activity detection as described above. The conditions are chosen such that stabilized variants show increased enzymatic activity relative to the parent after incubation on the detection media.

To screen for variants with altered thermostability, filters with bound variants are incubated in buffer at a given pH (e.g., in the range from pH 2-12) at an elevated temperature (e.g., in the range from 50°-110°C) for a time period (e.g., from 1-20 minutes) to inactivate nearly all of the parent pullulanase, rinsed in water, then placed directly on a detection plate containing immobilized Cibacron Blue labeled pullulan and incubated until activity is detectable. As will be

understood, thermostability and increased isoamylase activity may be tested simultaneously by using a detection plate containing immobilized Cibacron Red labeled amylopectin and incubate until activity is detectable. Moreover, pH dependent stability can be screened for by adjusting the pH of the buffer in the above inactivation step such that the parent pullulanase is inactivated, thereby allowing detection of only those variants with increased stability at the pH in question. To screen for variants with increased calcium-dependent stability, calcium chelators, such as ethylene glycol-bis(beta-aminoethyl ether) N,N,N',N'-tetraacetic acid (EGTA), is added to the inactivation buffer at a concentration such that the parent pullulanase is inactivated under conditions further defined, such as buffer pH, temperature or a specified length of incubation.

The variants of the invention may be suitably tested by assaying the pullulan- or amylopectin-degrading activity of the variant, for instance by growing host cells transformed with a DNA sequence encoding a variant on a starch-containing agarose plate and identifying pullulan- and/or amylopectin-degrading host cells as described above. Further testing in regard to altered properties, including specific activity, substrate specificity, cleavage pattern, thermoactivation, thermostability, pH dependent activity or optimum, pH dependent stability, temperature dependent activity or optimum, transglycosylation activity, stability, and any other parameter of interest, may be performed on purified variants in accordance with methods known in the art as described below.

Finally the present invention relates to the used of a pullulanase variant of the invention for starch conversion, both for the liquefaction and saccharification steps, in particular for producing syrups, such as dextrose or maltose syrups. A pullulanase variant of the invention may also be used for producing sweeteners; ethanol, such as fuel, drinking and industrial ethanol, from starch or whole grains (see for instance US patent no. 5,231,017-A or US patent no. 5,756,714-A hereby incorporated by reference). Further, a pullulanase variant of the invention may also be used as cleaning

ingredient, in laundry detergent compositions, dishwashing detergent, and hard surface cleaning compositions (see e.g., WO 99/23211, WO 97/07202 or WO 96/238874 for details on examples on cleaning compositions ingredients, the references hereby being incorporated by reference). Normally a cleaning or detergent composition also comprises at least a protease, in particular *Bacillus* proteases, and also one or more of the following activities: alpha-amylase, lipase, cellulase, mannanase, CGTase, maltogenic amylase.

The invention is further illustrated with reference to the following examples that are not intended to be in any way limiting to the scope of the invention as claimed.

Determination of pullulanase activity

Endo-pullulanase activity in NPUN is measured relative to a Novozymes pullulanase standard. One pullulanase unit (NPUN) is defined as the amount of enzyme that releases 1 micro mol glucose per minute under the standard conditions (0.7% red pullulan (Megazyme), pH 5, 40°C, 20 minutes). The activity is measured in NPUN/ml using red pullulan.

1 ml diluted sample or standard is incubated at 40°C for 2 minutes. 0.5 ml 2% red pullulan, 0.5 M KCl, 50 mM citric acid, pH 5 are added and mixed. The tubes are incubated at 40°C for 20 minutes and stopped by adding 2.5 ml 80% ethanol. The tubes are left standing at room temperature for 10-60 minutes followed by centrifugation 10 minutes at 4000 rpm. OD of the supernatants is then measured at 510 nm and the activity calculated using a standard curve.

Expression of pullulanase from *Bacillus deramificans*

The pullulanase from *Bacillus deramificans* (SEQ ID NO: 3) is expressed in *B. subtilis* from a plasmid denoted pCA36. This plasmid contains the complete gene encoding the pullulanase, the expression of which is directed by the promoter from *Bacillus amyloliquefaciens* alpha-amylase. Further, the plasmid contains the origin of replication, *oriT*, from plasmid pUB110 and the *cat* gene from plasmid pC194 conferring resistance towards chloramphenicol. PCA36 is shown in Fig. 1.

EXAMPLES

EXAMPLE 1

Construction of *Bacillus deramificans* D620A variant

Gene specific primer 132011 and mutagenic primer 132012 are used to amplify by PCR an approximately 410 bp DNA fragment from the pCA36 plasmid.

The 410 bp fragment is purified from an agarose gel and used as a Mega-primer together with primer 136054 in a second PCR carried out on the same template.

The resulting approximately 1110 bp fragment is digested with restriction enzymes BsiW I and Mlu I and the resulting approximately 330 bp DNA fragment is purified and ligated with the pCA36 plasmid digested with the same enzymes. Competent *Bacillus subtilis* SHA273 (amylase and protease low) cells are transformed with the ligation and chlorampenicol resistant transformants are checked by colony PCR.

The mutagenesis primer 132012 introduced the D620A substitution (written in bold in the primer sequence) and introduced simultaneously a Bgl I restriction site (underlined in the primer seq.), which facilitates easy pinpointing of mutants.

Finally, DNA sequencing was carried out to verify the presence of the correct mutations on the plasmid.

Primer 132011:
5' cgcttcggaatcattaggattgc 3' (SEQ ID NO: 7)
Primer 132012:
5' gcttccgttttgccttaatggcgctgc 3' (SEQ ID NO: 8)
Primer 136054:
5' ggccaaggctctacccgaacggc 3' (SEQ ID NO: 9)

EXAMPLE 2

Construction of *Bacillus deramificans* E649A variant

This variant constructed as described in Example 1, except that mutagenic primer 132013 is used. The mutagenesis primer 132013 introduced the E649A substitution (written in bold in the primer sequence) and a NarI restriction site

(underlined in the primer sequence), which facilitates easy pinpointing of mutants.

Primer 132013:
5' gcactttacgggcgccatggacggg 3' (SEQ ID NO: 10)

EXAMPLE 3

Thermostability test of variant of the invention

The below mentioned variants were constructed in *Bacillus deramificans* pullullanase using a megaprimer approach similar to the one described above. The following primers were used in order to introduce the various amino acid changes indicated below (all primer are written directional (5'-3'):

deletion (1-111)

Nr.167 TVB400: CATTCTGCAGCGGCCGCAAACGCTTATTTAGATGCTTCAAACC (SEQ ID NO: 11)

deletion(1-113)

Nr.168-tvb401: CATTCTGCAGCGGCCGCAGATGATCTTGGGAATACCTATAC (SEQ ID NO: 12)

D562P

Nr.170-tvb496:CTTTGCCACGCAGATCTCTCCCTTCGATAAAATTG (SEQ ID NO: 13)

G292P

NR.171-tvb497:CATTCAAACGGATCCCTATCAGGCAAAG (SEQ ID NO: 14)

G794P

Nr.172-tvb498:GTTATAATGCACCCGATGCGGTCAATG (SEQ ID NO: 15)

D148P

Nr. 173-tvb499:CAGCAAATAAGCCCATTCCAGTGACATCTGTG (SEQ ID NO: 16)

N119P

Nr. 174-tvb500:CTTATTTAGATGCATCACCCCAGGTGC (SEQ ID NO: 17)

N400S

Nr.175-tvb567:CAACTGCGATCGCACCAAGTGGAACGAG (SEQ ID NO: 18)

N400L

Nr.176-tvb568:GCGATCGCACCACTTGGAACGAGAGGC (SEQ ID NO: 19)

N400F

Nr.177-tvb569:CTGCGATCGCACCATTTGGAACGAGAGGC (SEQ ID NO: 20)

N446S

Nr.178-tvb570:GACTTTTCAATTGACCCTTCTTCGGGTAT (SEQ ID NO: 21)

N446L

Nr.179-tvb571:GTCCGTGACTTTTCAATTGACCCTCTTTCGGG (SEQ ID NO: 22)

N446F

Nr.180-tvb572:GTCCGTGACTTTTCAATTGACCCTTTTTCGGGTATG (SEQ ID NO: 23)

N504S

Nr.181-tvb573:CCAAGATAGTTGGGGTTACGATCCTCGCAAC (SEQ ID NO: 24)

N504L

Nr.182-tvb574:CCAAGATCTTTGGGGTTACGATCCTCGC (SEQ ID NO: 25)

N504F

Nr.183-tvb575:CCCAAGATTTTTGGGGTTACGATCCTCGC (SEQ ID NO: 26)

N735S

Nr.184-tvb576:GTCACAAGTCACGATAGCTACACCCTTTGGG (SEQ ID NO: 27)

N735L

Nr.185-tvb577:GTCACAAGTCACGATCTCTACACCCTTTGGGAC (SEQ ID NO: 28)

N735F

Nr.186-tvb578:GTCACAAGTCACGATTTCTACACCCTTTGGG (SEQ ID NO: 29)

N789S

Nr.187-tvb579:GCAACGACAGTAGTTATAATGCCGGCGATG (SEQ ID NO: 30)

N789L

Nr.188-tvb580 GCAACGACCTTAGTTATAATGCCGGCGATG (SEQ ID NO: 31)

N789F

Nr.189-tvb581 GCAACGACTTTAGTTATAATGCCGGCGATG (SEQ ID NO: 32)

I566A

Nr.190-TVB582 GACTTCGATAAAGCGGTACCAGAATATTATTACC (SEQ ID NO: 33)

Q485H

Nr. 191 TVB 583 GGGATTACACATGTTCATCTTATGCCTGTTTTCG (SEQ ID NO: 34)

V551I

Nr. 192 TVB 584 CATTGGGGTCAACATGGATGTTATCTATAATCATACC (SEQ ID NO: 35)

S492F

Nr. 193 TVB 585 GTTTTCGCATTTAACAGTGTCGACGAAACTGATCC (SEQ ID NO: 36)

D444R

Nr. 194 TVB 586 GACTTTTCCATTCGCCCGAATTCGGGTATG (SEQ ID NO: 37)

D444K

Nr 195 TVB 587 CGTGACTTTTCCATTAAACCGAATTCGGGTATG (SEQ ID NO: 38)

The deletion of an internal fragment corresponding to amino acids 154 to amino acid 273 was done by SOE PCR (Horton et al, 1989, Gene 77: pp61-68) utilizing the following two overlap generating oligonucleotides:

1) CCCTAGAGTAACAGATGTCACTGGAATATCC (SEQ ID NO: 39)

2)GGATATTCCAGTGACATCTGTTACTCTAGGGG (SEQ ID NO: 40)

Bacillus subtilis SHA273 was transformed with plasmids harbouring the various variants and fermented.

The fermentation supernatant containing pullulanase variant is subjected to the stability assay (Thermostability Assay 2 (T½)) in order to determine T½ values of inactivation using the assay described above.

1	N	PRO	A	112	80.159	5.264	-8.274	1.00	42.79
2	CA	PRO	A	112	79.045	4.605	-7.604	1.00	41.43
3	C	PRO	A	112	79.488	3.326	-6.903	1.00	39.90
4	O	PRO	A	112	80.510	2.695	-7.236	1.00	39.13
5	CB	PRO	A	112	78.020	4.300	-8.676	1.00	41.58
6	CG	PRO	A	112	78.845	4.164	-9.902	1.00	42.58
7	CD	PRO	A	112	79.947	5.166	-9.749	1.00	43.50
8	N	SER	A	113	78.659	2.987	-5.901	1.00	36.72
9	CA	SER	A	113	79.034	1.812	-5.120	1.00	35.45
10	C	SER	A	113	77.884	0.992	-4.544	1.00	33.99
11	O	SER	A	113	76.732	1.456	-4.501	1.00	33.34
12	CB	SER	A	113	79.793	2.427	-3.932	1.00	36.77
13	OG	SER	A	113	78.763	3.023	-3.107	1.00	37.94
14	N	VAL	A	114	78.232	-0.222	-4.096	1.00	30.90
15	CA	VAL	A	114	77.141	-0.914	-3.375	1.00	31.03
16	C	VAL	A	114	77.274	-0.292	-1.972	1.00	29.16
17	O	VAL	A	114	78.389	-0.274	-1.420	1.00	31.09
18	CB	VAL	A	114	77.417	-2.419	-3.553	1.00	31.41
19	CG1	VAL	A	114	76.525	-3.253	-2.635	1.00	30.36
20	CG2	VAL	A	114	77.488	-3.080	-4.917	1.00	30.56
21	N	SER	A	115	76.266	0.401	-1.479	1.00	27.09
22	CA	SER	A	115	76.390	1.084	-0.183	1.00	25.38
23	C	SER	A	115	76.091	0.149	0.997	1.00	24.90
24	O	SER	A	115	76.347	0.637	2.117	1.00	24.00
25	CB	SER	A	115	75.558	2.373	-0.187	1.00	22.77
26	OG	SER	A	115	74.201	2.001	-0.328	1.00	22.64
27	N	ASN	A	116	75.460	-0.989	0.840	1.00	23.19
28	CA	ASN	A	116	75.223	-1.897	1.968	1.00	22.52
29	C	ASN	A	116	74.830	-3.257	1.420	1.00	21.30
30	O	ASN	A	116	74.230	-3.250	0.354	1.00	20.56
31	CB	ASN	A	116	74.117	-1.373	2.885	1.00	23.16
32	CG	ASN	A	116	74.004	-2.136	4.191	1.00	21.84
33	OD1	ASN	A	116	74.777	-1.866	5.122	1.00	20.82
34	ND2	ASN	A	116	73.090	-3.083	4.280	1.00	20.73
35	N	ALA	A	117	75.230	-4.313	2.098	1.00	19.74
36	CA	ALA	A	117	74.843	-5.672	1.740	1.00	19.18
37	C	ALA	A	117	74.602	-6.504	3.002	1.00	20.75
38	O	ALA	A	117	75.366	-6.467	3.957	1.00	21.21
39	CB	ALA	A	117	75.831	-6.457	0.873	1.00	17.81
40	N	TYR	A	118	73.479	-7.242	2.937	1.00	19.90
41	CA	TYR	A	118	73.080	-8.099	4.042	1.00	20.50
42	C	TYR	A	118	72.917	-9.549	3.578	1.00	19.96
43	O	TYR	A	118	72.422	-9.839	2.494	1.00	22.33
44	CB	TYR	A	118	71.739	-7.589	4.569	1.00	20.09
45	CG	TYR	A	118	71.932	-6.424	5.476	1.00	18.77
46	CD1	TYR	A	118	73.008	-6.394	6.361	1.00	18.02
47	CD2	TYR	A	118	70.931	-5.460	5.586	1.00	17.79
48	CE1	TYR	A	118	73.073	-5.426	7.355	1.00	17.37
49	CE2	TYR	A	118	70.987	-4.499	6.586	1.00	17.81
50	CZ	TYR	A	118	72.050	-4.480	7.470	1.00	17.70
51	OH	TYR	A	118	72.116	-3.520	8.458	1.00	16.31
52	N	LEU	A	119	73.396	-10.483	4.417	1.00	17.54
53	CA	LEU	A	119	73.089	-11.871	4.133	1.00	17.55
54	C	LEU	A	119	71.822	-12.293	4.863	1.00	17.58
55	O	LEU	A	119	71.801	-12.501	6.070	1.00	16.85
56	CB	LEU	A	119	74.257	-12.745	4.571	1.00	17.57
57	CG	LEU	A	119	74.043	-14.215	4.193	1.00	20.46
58	CD1	LEU	A	119	73.879	-14.416	2.682	1.00	20.82
59	CD2	LEU	A	119	75.196	-15.116	4.624	1.00	21.33
60	N	ASP	A	120	70.677	-12.315	4.183	1.00	17.72
61	CA	ASP	A	120	69.372	-12.510	4.811	1.00	16.35
62	C	ASP	A	120	68.815	-13.933	4.760	1.00	17.71
63	O	ASP	A	120	67.794	-14.173	5.449	1.00	16.09
64	CB	ASP	A	120	68.314	-11.512	4.346	1.00	17.88
65	CG	ASP	A	120	68.469	-10.114	4.912	1.00	18.37
66	OD1	ASP	A	120	69.040	-9.909	5.994	1.00	17.74
67	OD2	ASP	A	120	68.000	-9.132	4.295	1.00	21.04
68	N	ASP	A	121	69.459	-14.847	4.069	1.00	16.19
69	CA	ASP	A	121	69.009	-16.253	4.082	1.00	19.25
70	C	ASP	A	121	70.291	-17.036	3.749	1.00	18.78
71	O	ASP	A	121	71.251	-16.347	3.404	1.00	16.73
72	CB	ASP	A	121	67.838	-16.599	3.188	1.00	18.82
73	CG	ASP	A	121	67.081	-17.860	3.551	1.00	21.17
74	OD1	ASP	A	121	65.897	-17.937	3.106	1.00	21.16
75	OD2	ASP	A	121	67.552	-18.838	4.190	1.00	19.81
76	N	GLU	A	122	70.312	-18.367	3.847	1.00	20.61
77	CA	GLU	A	122	71.613	-19.020	3.562	1.00	23.88
78	C	GLU	A	122	72.181	-18.700	2.193	1.00	21.23
79	O	GLU	A	122	73.415	-18.680	2.060	1.00	20.25
80	CB	GLU	A	122	71.517	-20.512	3.825	1.00	26.85
81	CG	GLU	A	122	70.813	-21.249	2.697	1.00	31.98
82	CD	GLU	A	122	70.644	-22.717	3.015	1.00	35.92
83	OE1	GLU	A	122	71.596	-23.371	3.499	1.00	38.33
84	OE2	GLU	A	122	69.534	-23.235	2.779	1.00	40.26
85	N	LYS	A	123	71.395	-18.480	1.147	1.00	21.26
86	CA	LYS	A	123	71.909	-18.121	-0.170	1.00	22.79
87	C	LYS	A	123	71.247	-16.879	-0.755	1.00	22.17
88	O	LYS	A	123	71.137	-16.788	-1.992	1.00	22.07
89	CB	LYS	A	123	71.655	-19.303	-1.115	1.00	24.69
90	CG	LYS	A	123	72.497	-20.528	-0.798	1.00	27.82
91	CD	LYS	A	123	71.837	-21.782	-1.305	1.00	30.95
92	CE	LYS	A	123	72.745	-22.985	-1.438	1.00	33.61
93	NZ	LYS	A	123	71.885	-24.227	-1.408	1.00	38.51

APPENDIX 1

94	N	THR	A	124	70.862	-15.914	0.062	1.00	18.31
95	CA	THR	A	124	70.223	-14.686	-0.397	1.00	19.05
96	C	THR	A	124	70.918	-13.424	0.117	1.00	19.03
97	O	THR	A	124	71.042	-13.313	1.342	1.00	18.19
98	CB	THR	A	124	68.759	-14.614	0.096	1.00	19.49
99	OG1	THR	A	124	68.093	-15.853	-0.273	1.00	21.02
100	CG2	THR	A	124	67.958	-13.436	-0.417	1.00	17.02
101	N	VAL	A	125	71.314	-12.463	-0.717	1.00	18.66
102	CA	VAL	A	125	71.852	-11.220	-0.221	1.00	20.11
103	C	VAL	A	125	70.971	-10.047	-0.698	1.00	20.51
104	O	VAL	A	125	70.485	-10.031	-1.819	1.00	21.45
105	CB	VAL	A	125	73.343	-10.945	-0.302	1.00	22.08
106	CG1	VAL	A	125	74.227	-12.123	-0.759	1.00	21.11
107	CG2	VAL	A	125	73.756	-9.615	-0.901	1.00	19.94
108	N	LEU	A	126	70.757	-9.068	0.176	1.00	19.28
109	CA	LEU	A	126	69.973	-7.883	-0.113	1.00	19.43
110	C	LEU	A	126	70.940	-6.717	-0.189	1.00	20.40
111	O	LEU	A	126	71.583	-6.433	0.840	1.00	17.65
112	CB	LEU	A	126	68.962	-7.679	1.033	1.00	19.40
113	CG	LEU	A	126	68.214	-6.352	0.939	1.00	21.05
114	CD1	LEU	A	126	67.147	-6.379	-0.146	1.00	17.96
115	CD2	LEU	A	126	67.643	-5.843	2.254	1.00	18.86
116	N	ALA	A	127	71.204	-6.161	-1.360	1.00	20.21
117	CA	ALA	A	127	72.232	-5.138	-1.506	1.00	23.09
118	C	ALA	A	127	71.665	-3.800	-1.965	1.00	24.49
119	O	ALA	A	127	70.837	-3.785	-2.898	1.00	24.26
120	CB	ALA	A	127	73.302	-5.630	-2.495	1.00	22.46
121	N	LYS	A	128	72.080	-2.709	-1.336	1.00	25.87
122	CA	LYS	A	128	71.568	-1.383	-1.764	1.00	27.63
123	C	LYS	A	128	72.616	-0.764	-2.712	1.00	27.55
124	O	LYS	A	128	73.804	-0.895	-2.438	1.00	24.66
125	CB	LYS	A	128	71.296	-0.455	-0.592	1.00	26.80
126	CG	LYS	A	128	70.839	0.946	-0.922	1.00	27.35
127	CD	LYS	A	128	69.376	1.128	-1.234	1.00	26.29
128	CE	LYS	A	128	69.084	2.556	-1.653	1.00	27.49
129	NZ	LYS	A	128	69.797	3.575	-0.866	1.00	29.77
130	N	LEU	A	129	72.178	-0.105	-3.777	1.00	29.12
131	CA	LEU	A	129	73.115	0.531	-4.714	1.00	29.81
132	C	LEU	A	129	73.067	2.052	-4.625	1.00	30.79
133	O	LEU	A	129	71.997	2.621	-4.412	1.00	29.69
134	CB	LEU	A	129	72.693	0.064	-6.092	1.00	29.38
135	CG	LEU	A	129	72.670	-1.425	-6.455	1.00	29.89
136	CD1	LEU	A	129	72.293	-1.585	-7.931	1.00	30.38
137	CD2	LEU	A	129	74.009	-2.112	-6.236	1.00	28.39
138	N	SER	A	130	74.162	2.782	-4.801	1.00	32.54
139	CA	SER	A	130	74.086	4.228	-4.641	1.00	34.33
140	C	SER	A	130	73.299	4.884	-5.773	1.00	36.79
141	O	SER	A	130	73.009	6.074	-5.768	1.00	37.29
142	CB	SER	A	130	75.512	4.788	-4.600	1.00	33.55
143	OG	SER	A	130	76.227	4.352	-5.759	1.00	34.68
144	N	MET	A	131	72.979	4.059	-6.795	1.00	37.15
145	CA	MET	A	131	72.225	4.581	-7.925	1.00	39.70
146	C	MET	A	131	71.602	3.473	-8.788	1.00	38.38
147	O	MET	A	131	72.036	2.331	-8.785	1.00	36.96
148	CB	MET	A	131	73.143	5.484	-8.760	1.00	42.16
149	CG	MET	A	131	74.218	4.719	-9.540	1.00	44.07
150	SD	MET	A	131	74.661	5.555	-11.071	1.00	48.37
151	CE	MET	A	131	76.298	6.126	-10.590	1.00	45.57
152	N	PRO	A	132	70.445	3.644	-9.407	1.00	38.54
153	CA	PRO	A	132	69.715	2.529	-9.985	1.00	38.36
154	C	PRO	A	132	70.487	1.983	-11.172	1.00	39.15
155	O	PRO	A	132	71.420	2.615	-11.696	1.00	39.25
156	CB	PRO	A	132	68.348	3.076	-10.341	1.00	39.31
157	CG	PRO	A	132	68.452	4.555	-10.271	1.00	39.22
158	CD	PRO	A	132	69.703	4.916	-9.513	1.00	39.47
159	N	MET	A	133	70.115	0.773	-11.554	1.00	38.46
160	CA	MET	A	133	70.680	0.062	-12.683	1.00	37.37
161	C	MET	A	133	69.465	-0.615	-13.315	1.00	38.14
162	O	MET	A	133	68.403	-0.628	-12.657	1.00	38.27
163	CB	MET	A	133	71.752	-0.962	-12.320	1.00	36.83
164	CG	MET	A	133	71.329	-2.070	-11.385	1.00	35.87
165	SD	MET	A	133	72.282	-3.590	-11.397	1.00	36.52
166	CE	MET	A	133	73.976	-3.108	-11.265	1.00	34.78
167	N	THR	A	134	69.598	-1.070	-14.564	1.00	38.11
168	CA	THR	A	134	68.453	-1.786	-15.145	1.00	37.87
169	C	THR	A	134	69.034	-3.203	-15.229	1.00	38.03
170	O	THR	A	134	70.166	-3.414	-15.685	1.00	35.72
171	CB	THR	A	134	67.747	-1.212	-16.362	1.00	39.56
172	OG1	THR	A	134	68.167	-1.836	-17.592	1.00	40.70
173	CG2	THR	A	134	67.867	0.296	-16.567	1.00	38.10
174	N	LEU	A	135	68.277	-4.155	-14.682	1.00	38.56
175	CA	LEU	A	135	68.779	-5.531	-14.645	1.00	38.93
176	C	LEU	A	135	68.807	-6.218	-16.003	1.00	40.69
177	O	LEU	A	135	67.927	-6.085	-16.837	1.00	40.85
178	CB	LEU	A	135	67.967	-6.330	-13.628	1.00	36.13
179	CG	LEU	A	135	67.915	-5.773	-12.197	1.00	33.81
180	CD1	LEU	A	135	66.758	-6.408	-11.456	1.00	33.44
181	CD2	LEU	A	135	69.218	-5.959	-11.427	1.00	31.63
182	N	ALA	A	136	69.851	-7.010	-16.203	1.00	42.89
183	CA	ALA	A	136	69.985	-7.876	-17.381	1.00	43.50
184	C	ALA	A	136	69.636	-9.277	-16.895	1.00	44.87
185	O	ALA	A	136	69.205	-9.395	-15.735	1.00	44.05
186	CB	ALA	A	136	71.376	-7.739	-17.952	1.00	42.02
187	N	ASP	A	137	69.783	-10.304	-17.719	1.00	45.61
188	CA	ASP	A	137	69.441	-11.652	-17.302	1.00	45.76
189	C	ASP	A	137	70.415	-12.326	-16.333	1.00	42.62

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190	O	ASP	A	137	71.558	-11.918	-16.176	1.00	41.07
191	CB	ASP	A	137	69.547	-12.644	-18.479	1.00	49.36
192	CG	ASP	A	137	68.263	-12.743	-19.277	1.00	52.75
193	OD1	ASP	A	137	68.067	-11.851	-20.128	1.00	54.23
194	OD2	ASP	A	137	67.474	-13.687	-19.039	1.00	54.86
195	N	ALA	A	138	69.898	-13.417	-15.742	1.00	40.77
196	CA	ALA	A	138	70.755	-14.138	-14.777	1.00	39.52
197	C	ALA	A	138	71.379	-13.240	-13.678	1.00	37.28
198	O	ALA	A	138	70.708	-12.438	-13.041	1.00	35.69
199	CB	ALA	A	138	71.862	-14.845	-15.560	1.00	38.20
200	N	ALA	A	139	72.686	-13.513	-13.520	1.00	34.74
201	CA	ALA	A	139	73.425	-12.724	-12.554	1.00	35.56
202	C	ALA	A	139	73.532	-11.183	-12.677	1.00	35.73
203	O	ALA	A	139	73.900	-10.477	-11.730	1.00	35.31
204	CB	ALA	A	139	74.919	-13.209	-12.589	1.00	34.52
205	N	SER	A	140	73.342	-10.684	-13.897	1.00	33.61
206	CA	SER	A	140	73.339	-9.259	-14.191	1.00	31.82
207	C	SER	A	140	74.597	-8.519	-13.797	1.00	30.11
208	O	SER	A	140	74.538	-7.393	-13.302	1.00	28.60
209	CB	SER	A	140	72.075	-8.690	-13.546	1.00	32.25
210	OG	SER	A	140	71.767	-7.352	-13.873	1.00	33.30
211	N	GLY	A	141	75.769	-9.122	-13.958	1.00	30.48
212	CA	GLY	A	141	77.065	-8.569	-13.643	1.00	29.15
213	C	GLY	A	141	77.524	-8.599	-12.198	1.00	30.03
214	O	GLY	A	141	78.613	-8.120	-11.877	1.00	29.74
215	N	PHE	A	142	76.701	-9.126	-11.278	1.00	29.58
216	CA	PHE	A	142	77.047	-9.134	-9.867	1.00	27.65
217	C	PHE	A	142	78.017	-10.281	-9.612	1.00	28.38
218	O	PHE	A	142	77.839	-11.354	-10.191	1.00	28.16
219	CB	PHE	A	142	75.796	-9.311	-8.977	1.00	25.35
220	CG	PHE	A	142	74.956	-8.071	-8.790	1.00	24.90
221	CD1	PHE	A	142	75.222	-7.188	-7.760	1.00	25.18
222	CD2	PHE	A	142	73.892	-7.778	-9.620	1.00	24.79
223	CE1	PHE	A	142	74.496	-6.026	-7.579	1.00	25.01
224	CE2	PHE	A	142	73.144	-6.628	-9.448	1.00	25.31
225	CZ	PHE	A	142	73.437	-5.749	-8.425	1.00	24.62
226	N	THR	A	143	78.971	-10.095	-8.696	1.00	28.09
227	CA	THR	A	143	79.811	-11.224	-8.292	1.00	29.96
228	C	THR	A	143	79.908	-11.299	-6.764	1.00	28.75
229	O	THR	A	143	79.791	-10.273	-6.092	1.00	30.13
230	CB	THR	A	143	81.234	-11.093	-8.857	1.00	30.83
231	OG1	THR	A	143	81.625	-9.746	-8.536	1.00	32.43
232	CG2	THR	A	143	81.348	-11.292	-10.365	1.00	31.64
233	N	VAL	A	144	80.192	-12.468	-6.219	1.00	27.73
234	CA	VAL	A	144	80.403	-12.603	-4.774	1.00	26.92
235	C	VAL	A	144	81.718	-13.339	-4.556	1.00	27.73
236	O	VAL	A	144	81.994	-14.337	-5.233	1.00	27.48
237	CB	VAL	A	144	79.255	-13.330	-4.060	1.00	24.80
238	CG1	VAL	A	144	79.645	-13.759	-2.633	1.00	24.36
239	CG2	VAL	A	144	78.034	-12.421	-3.949	1.00	24.13
240	N	ILE	A	145	82.561	-12.879	-3.637	1.00	28.05
241	CA	ILE	A	145	83.791	-13.551	-3.267	1.00	28.41
242	C	ILE	A	145	83.948	-13.647	-1.740	1.00	28.01
243	O	ILE	A	145	83.742	-12.756	-0.920	1.00	25.69
244	CB	ILE	A	145	85.080	-12.944	-3.871	1.00	31.57
245	CG1	ILE	A	145	85.020	-12.914	-5.399	1.00	34.81
246	CG2	ILE	A	145	86.300	-13.815	-3.542	1.00	31.61
247	CD1	ILE	A	145	85.691	-11.801	-6.162	0.00	38.05
248	N	ASP	A	146	84.373	-14.837	-1.350	1.00	25.58
249	CA	ASP	A	146	84.778	-15.165	0.006	1.00	28.42
250	C	ASP	A	146	86.263	-14.824	0.057	1.00	28.22
251	O	ASP	A	146	87.082	-15.643	-0.371	1.00	27.06
252	CB	ASP	A	146	84.462	-16.636	0.239	1.00	26.87
253	CG	ASP	A	146	84.854	-17.200	1.576	1.00	28.99
254	OD1	ASP	A	146	85.512	-16.536	2.398	1.00	27.91
255	OD2	ASP	A	146	84.521	-18.391	1.822	1.00	28.00
256	N	LYS	A	147	86.657	-13.694	0.591	1.00	29.63
257	CA	LYS	A	147	88.035	-13.237	0.631	1.00	33.19
258	C	LYS	A	147	88.933	-14.018	1.577	1.00	33.69
259	O	LYS	A	147	90.160	-13.941	1.450	1.00	33.61
260	CB	LYS	A	147	88.113	-11.724	0.937	1.00	35.09
261	CG	LYS	A	147	87.594	-10.845	-0.194	1.00	37.87
262	CD	LYS	A	147	88.354	-9.540	-0.293	1.00	39.84
263	CE	LYS	A	147	88.103	-8.652	0.904	1.00	43.26
264	NZ	LYS	A	147	88.602	-7.248	0.739	1.00	45.31
265	N	THR	A	148	88.360	-14.796	2.487	1.00	31.96
266	CA	THR	A	148	89.108	-15.593	3.444	1.00	30.46
267	C	THR	A	148	89.841	-16.711	2.711	1.00	32.06
268	O	THR	A	148	91.043	-16.921	2.873	1.00	30.77
269	CB	THR	A	148	88.182	-16.136	4.545	1.00	28.74
270	OG1	THR	A	148	87.559	-15.026	5.205	1.00	25.09
271	CG2	THR	A	148	88.854	-16.928	5.658	1.00	29.31
272	N	THR	A	149	89.131	-17.425	1.847	1.00	31.51
273	CA	THR	A	149	89.650	-18.565	1.097	1.00	32.38
274	C	THR	A	149	90.032	-18.207	-0.336	1.00	34.28
275	O	THR	A	149	90.843	-18.860	-0.978	1.00	34.35
276	CB	THR	A	149	88.573	-19.672	1.002	1.00	31.79
277	OG1	THR	A	149	87.433	-19.098	0.347	1.00	31.53
278	CG2	THR	A	149	88.174	-20.139	2.387	1.00	31.56
279	N	GLY	A	150	89.415	-17.156	-0.867	1.00	34.16
280	CA	GLY	A	150	89.621	-16.692	-2.232	1.00	35.07
281	C	GLY	A	150	88.528	-17.240	-3.148	1.00	34.60
282	O	GLY	A	150	88.453	-16.846	-4.298	1.00	34.70
283	N	GLU	A	151	87.706	-18.163	-2.651	1.00	34.79
284	CA	GLU	A	151	86.647	-18.768	-3.457	1.00	36.01
285	C	GLU	A	151	85.618	-17.746	-3.946	1.00	35.57

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286	O	GLU	A	151	85.046	-16.957	-3.184	1.00	32.89
287	CB	GLU	A	151	85.878	-19.866	-2.699	1.00	36.86
288	CG	GLU	A	151	84.457	-20.388	-2.912	1.00	39.81
289	CD	GLU	A	151	83.800	-21.357	-1.955	1.00	41.00
290	OE1	GLU	A	151	83.941	-21.618	-0.761	1.00	20.00
291	OE2	GLU	A	151	82.953	-21.888	-2.659	1.00	20.00
292	N	LYS	A	152	85.373	-17.792	-5.258	1.00	34.10
293	CA	LYS	A	152	84.388	-16.920	-5.880	1.00	33.14
294	C	LYS	A	152	83.100	-17.721	-5.895	1.00	32.88
295	O	LYS	A	152	83.174	-18.923	-6.156	1.00	34.46
296	CB	LYS	A	152	84.713	-16.397	-7.291	1.00	33.96
297	CG	LYS	A	152	86.053	-15.890	-7.831	1.00	20.00
298	CD	LYS	A	152	86.300	-15.397	-9.258	1.00	20.00
299	CE	LYS	A	152	87.720	-14.878	-9.009	1.00	20.00
300	NZ	LYS	A	152	88.820	-14.900	-9.971	1.00	20.00
301	N	ILE	A	153	81.971	-17.105	-5.571	1.00	30.39
302	CA	ILE	A	153	80.697	-17.797	-5.515	1.00	30.58
303	C	ILE	A	153	79.726	-17.261	-6.561	1.00	30.18
304	O	ILE	A	153	79.369	-16.087	-6.544	1.00	29.54
305	CB	ILE	A	153	80.079	-17.596	-4.102	1.00	30.99
306	CG1	ILE	A	153	81.005	-18.163	-3.015	1.00	32.60
307	CG2	ILE	A	153	78.708	-18.243	-4.058	1.00	30.51
308	CD1	ILE	A	153	80.665	-17.636	-1.620	1.00	33.71
309	N	PRO	A	154	79.304	-18.086	-7.516	1.00	30.89
310	CA	PRO	A	154	78.425	-17.617	-8.577	1.00	29.91
311	C	PRO	A	154	77.070	-17.092	-8.125	1.00	29.11
312	O	PRO	A	154	76.389	-17.689	-7.291	1.00	28.76
313	CB	PRO	A	154	78.239	-18.829	-9.471	1.00	30.32
314	CG	PRO	A	154	79.208	-19.853	-9.041	1.00	31.95
315	CD	PRO	A	154	79.709	-19.499	-7.665	1.00	30.13
316	N	VAL	A	155	76.635	-15.979	-8.687	1.00	29.63
317	CA	VAL	A	155	75.325	-15.376	-8.443	1.00	30.78
318	C	VAL	A	155	74.378	-15.940	-9.509	1.00	30.85
319	O	VAL	A	155	74.696	-15.745	-10.690	1.00	30.08
320	CB	VAL	A	155	75.011	-13.871	-8.530	1.00	30.85
321	CG1	VAL	A	155	73.695	-13.215	-8.115	1.00	20.00
322	CG2	VAL	A	155	76.117	-13.400	-7.604	1.00	29.33
323	N	THR	A	156	73.320	-16.648	-9.159	1.00	29.83
324	CA	THR	A	156	72.450	-17.270	-10.144	1.00	31.67
325	C	THR	A	156	71.245	-16.427	-10.562	1.00	32.89
326	O	THR	A	156	70.632	-16.699	-11.621	1.00	32.33
327	CB	THR	A	156	71.956	-18.634	-9.635	1.00	31.70
328	OG1	THR	A	156	71.092	-18.419	-8.515	1.00	31.91
329	CG2	THR	A	156	73.150	-19.479	-9.186	1.00	32.24
330	N	SER	A	157	70.880	-15.436	-9.730	1.00	31.06
331	CA	SER	A	157	69.833	-14.506	-10.141	1.00	30.56
332	C	SER	A	157	69.803	-13.227	-9.308	1.00	29.60
333	O	SER	A	157	70.337	-13.169	-8.195	1.00	27.35
334	CB	SER	A	157	68.491	-15.222	-10.214	1.00	32.34
335	OG	SER	A	157	67.810	-15.173	-9.012	1.00	35.08
336	N	ALA	A	158	69.446	-12.117	-9.959	1.00	26.45
337	CA	ALA	A	158	69.453	-10.774	-9.423	1.00	27.24
338	C	ALA	A	158	68.152	-10.053	-9.765	1.00	30.18
339	O	ALA	A	158	67.765	-9.918	-10.959	1.00	30.53
340	CB	ALA	A	158	70.645	-10.022	-9.985	1.00	26.36
341	N	VAL	A	159	67.340	-9.812	-8.734	1.00	28.12
342	CA	VAL	A	159	66.000	-9.269	-8.930	1.00	28.80
343	C	VAL	A	159	65.789	-8.029	-8.074	1.00	28.52
344	O	VAL	A	159	66.627	-7.709	-7.226	1.00	25.60
345	CB	VAL	A	159	64.846	-10.243	-8.667	1.00	29.04
346	CG1	VAL	A	159	64.965	-11.513	-9.494	1.00	29.16
347	CG2	VAL	A	159	64.667	-10.636	-7.188	1.00	27.70
348	N	SER	A	160	64.643	-7.357	-8.283	1.00	28.60
349	CA	SER	A	160	64.422	-6.159	-7.460	1.00	27.56
350	C	SER	A	160	63.738	-6.562	-6.141	1.00	27.31
351	O	SER	A	160	62.904	-7.468	-6.153	1.00	25.37
352	CB	SER	A	160	63.626	-5.076	-8.149	1.00	28.21
353	OG	SER	A	160	63.262	-4.072	-7.188	1.00	25.98
354	N	ALA	A	161	64.205	-5.955	-5.033	1.00	25.91
355	CA	ALA	A	161	63.629	-6.241	-3.731	1.00	25.68
356	C	ALA	A	161	62.547	-5.238	-3.329	1.00	26.62
357	O	ALA	A	161	61.886	-5.395	-2.296	1.00	23.95
358	CB	ALA	A	161	64.715	-6.344	-2.642	1.00	25.65
359	N	ASN	A	162	62.257	-4.216	-4.131	1.00	26.84
360	CA	ASN	A	162	61.183	-3.278	-3.763	1.00	27.62
361	C	ASN	A	162	59.841	-3.987	-3.818	1.00	28.07
362	O	ASN	A	162	59.547	-4.755	-4.741	1.00	28.17
363	CB	ASN	A	162	61.196	-2.092	-4.718	1.00	28.34
364	CG	ASN	A	162	62.395	-1.174	-4.643	1.00	29.74
365	OD1	ASN	A	162	62.886	-0.911	-3.535	1.00	30.40
366	ND2	ASN	A	162	62.829	-0.625	-5.774	1.00	27.62
367	N	PRO	A	163	58.979	-3.767	-2.828	1.00	27.79
368	CA	PRO	A	163	57.661	-4.372	-2.786	1.00	26.20
369	C	PRO	A	163	56.742	-3.804	-3.860	1.00	25.38
370	O	PRO	A	163	56.967	-2.735	-4.449	1.00	24.29
371	CB	PRO	A	163	57.181	-4.066	-1.369	1.00	27.88
372	CG	PRO	A	163	57.870	-2.776	-1.027	1.00	28.89
373	CD	PRO	A	163	59.234	-2.875	-1.661	1.00	27.81
374	N	VAL	A	164	55.717	-4.569	-4.208	1.00	25.30
375	CA	VAL	A	164	54.721	-4.187	-5.220	1.00	25.51
376	C	VAL	A	164	53.339	-4.283	-4.585	1.00	24.80
377	O	VAL	A	164	52.995	-5.340	-4.040	1.00	26.11
378	CB	VAL	A	164	54.802	-5.048	-6.493	1.00	24.71
379	CG1	VAL	A	164	53.663	-4.752	-7.467	1.00	26.19
380	CG2	VAL	A	164	56.125	-4.811	-7.253	1.00	25.42
381	N	THR	A	165	52.538	-3.233	-4.606	1.00	24.33

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382	CA	THR	A	165	51.200	-3.270	-4.032	1.00	25.19
383	C	THR	A	165	50.176	-3.008	-5.166	1.00	24.41
384	O	THR	A	165	49.956	-1.847	-5.503	1.00	21.40
385	CB	THR	A	165	50.966	-2.262	-2.897	1.00	26.83
386	OG1	THR	A	165	51.832	-2.523	-1.774	1.00	28.11
387	CG2	THR	A	165	49.533	-2.347	-2.377	1.00	25.74
388	N	ALA	A	166	49.546	-4.081	-5.643	1.00	22.25
389	CA	ALA	A	166	48.656	-3.909	-6.820	1.00	23.36
390	C	ALA	A	166	47.323	-4.512	-6.453	1.00	22.56
391	O	ALA	A	166	47.351	-5.703	-6.108	1.00	24.73
392	CB	ALA	A	166	49.294	-4.589	-8.031	1.00	19.57
393	N	VAL	A	167	46.229	-3.768	-6.464	1.00	22.47
394	CA	VAL	A	167	44.939	-4.309	-6.043	1.00	19.46
395	C	VAL	A	167	43.980	-4.333	-7.248	1.00	21.03
396	O	VAL	A	167	43.901	-3.309	-7.917	1.00	18.72
397	CB	VAL	A	167	44.310	-3.476	-4.911	1.00	20.70
398	CG1	VAL	A	167	42.832	-3.503	-4.525	1.00	18.70
399	CG2	VAL	A	167	45.155	-3.486	-3.651	1.00	22.11
400	N	LEU	A	168	43.264	-5.454	-7.447	1.00	19.41
401	CA	LEU	A	168	42.257	-5.482	-8.519	1.00	18.94
402	C	LEU	A	168	41.053	-4.647	-8.099	1.00	20.89
403	O	LEU	A	168	40.431	-4.955	-7.048	1.00	21.09
404	CB	LEU	A	168	41.808	-6.925	-8.770	1.00	18.27
405	CG	LEU	A	168	40.646	-7.136	-9.739	1.00	18.57
406	CD1	LEU	A	168	41.115	-6.720	-11.135	1.00	17.67
407	CD2	LEU	A	168	40.166	-8.607	-9.767	1.00	17.71
408	N	VAL	A	169	40.726	-3.598	-8.865	1.00	20.18
409	CA	VAL	A	169	39.571	-2.758	-8.519	1.00	19.68
410	C	VAL	A	169	38.501	-2.816	-9.592	1.00	20.02
411	O	VAL	A	169	38.871	-2.925	-10.765	1.00	19.91
412	CB	VAL	A	169	39.943	-1.260	-8.324	1.00	19.72
413	CG1	VAL	A	169	40.903	-1.142	-7.131	1.00	17.22
414	CG2	VAL	A	169	40.600	-0.612	-9.541	1.00	18.93
415	N	GLY	A	170	37.224	-2.742	-9.246	1.00	18.55
416	CA	GLY	A	170	36.172	-2.790	-10.248	1.00	18.73
417	C	GLY	A	170	34.791	-3.031	-9.664	1.00	17.66
418	O	GLY	A	170	34.639	-3.096	-8.438	1.00	17.25
419	N	ASP	A	171	33.806	-3.317	-10.500	1.00	18.35
420	CA	ASP	A	171	32.470	-3.653	-10.006	1.00	22.28
421	C	ASP	A	171	32.356	-5.172	-9.771	1.00	22.87
422	O	ASP	A	171	31.275	-5.671	-9.490	1.00	21.75
423	CB	ASP	A	171	31.304	-3.164	-10.866	1.00	22.13
424	CG	ASP	A	171	31.364	-3.728	-12.276	1.00	24.79
425	OD1	ASP	A	171	32.272	-4.532	-12.592	1.00	24.08
426	OD2	ASP	A	171	30.463	-3.373	-13.068	1.00	25.44
427	N	LEU	A	172	33.459	-5.907	-9.824	1.00	23.38
428	CA	LEU	A	172	33.556	-7.317	-9.519	1.00	23.45
429	C	LEU	A	172	34.101	-7.426	-8.093	1.00	23.46
430	O	LEU	A	172	34.338	-8.531	-7.601	1.00	23.89
431	CB	LEU	A	172	34.488	-8.066	-10.492	1.00	23.96
432	CG	LEU	A	172	35.716	-7.388	-11.089	1.00	23.60
433	CD1	LEU	A	172	36.700	-6.874	-10.024	1.00	23.92
434	CD2	LEU	A	172	36.501	-8.286	-12.049	1.00	22.64
435	N	GLN	A	173	34.427	-6.304	-7.425	1.00	22.02
436	CA	GLN	A	173	35.116	-6.409	-6.144	1.00	23.00
437	C	GLN	A	173	34.301	-7.061	-5.012	1.00	25.30
438	O	GLN	A	173	34.956	-7.770	-4.222	1.00	23.45
439	CB	GLN	A	173	35.715	-5.085	-5.640	1.00	19.82
440	CG	GLN	A	173	37.222	-5.133	-5.502	1.00	20.64
441	CD	GLN	A	173	37.865	-3.790	-5.190	1.00	20.89
442	OE1	GLN	A	173	38.776	-3.712	-4.337	1.00	21.68
443	NE2	GLN	A	173	37.472	-2.762	-5.917	1.00	14.10
444	N	GLN	A	174	33.011	-6.766	-4.897	1.00	27.15
445	CA	GLN	A	174	32.211	-7.350	-3.808	1.00	30.17
446	C	GLN	A	174	32.010	-8.853	-3.980	1.00	29.95
447	O	GLN	A	174	32.162	-9.617	-3.030	1.00	29.74
448	CB	GLN	A	174	30.806	-6.738	-3.686	1.00	30.31
449	CG	GLN	A	174	30.791	-5.300	-3.184	1.00	31.02
450	CD	GLN	A	174	29.381	-4.727	-3.153	1.00	32.11
451	OE1	GLN	A	174	28.641	-4.750	-4.123	1.00	32.20
452	NE2	GLN	A	174	29.058	-4.103	-2.011	1.00	32.45
453	N	ALA	A	175	31.859	-9.290	-5.225	1.00	30.17
454	CA	ALA	A	175	31.793	-10.722	-5.537	1.00	30.64
455	C	ALA	A	175	33.072	-11.450	-5.174	1.00	30.81
456	O	ALA	A	175	33.044	-12.667	-4.926	1.00	31.59
457	CB	ALA	A	175	31.469	-10.864	-7.023	1.00	30.89
458	N	LEU	A	176	34.188	-10.738	-5.050	1.00	29.83
459	CA	LEU	A	176	35.474	-11.299	-4.683	1.00	30.69
460	C	LEU	A	176	35.799	-11.058	-3.218	1.00	31.12
461	O	LEU	A	176	36.912	-11.315	-2.771	1.00	31.07
462	CB	LEU	A	176	36.587	-10.806	-5.622	1.00	30.20
463	CG	LEU	A	176	36.490	-11.210	-7.098	1.00	30.54
464	CD1	LEU	A	176	37.534	-10.515	-7.971	1.00	28.99
465	CD2	LEU	A	176	36.726	-12.713	-7.263	1.00	30.40
466	N	GLY	A	177	34.829	-10.590	-2.432	1.00	33.38
467	CA	GLY	A	177	34.977	-10.426	-1.004	1.00	34.48
468	C	GLY	A	177	35.277	-9.040	-0.468	1.00	36.08
469	O	GLY	A	177	35.331	-8.865	0.764	1.00	35.24
470	N	ALA	A	178	35.543	-8.079	-1.354	1.00	34.40
471	CA	ALA	A	178	35.818	-6.733	-0.871	1.00	34.80
472	C	ALA	A	178	34.509	-6.155	-0.321	1.00	33.76
473	O	ALA	A	178	33.439	-6.440	-0.842	1.00	33.43
474	CB	ALA	A	178	36.359	-5.829	-1.970	1.00	32.96
475	N	ALA	A	179	34.601	-5.282	0.670	1.00	33.57
476	CA	ALA	A	179	33.434	-4.614	1.223	1.00	32.22
477	C	ALA	A	179	32.707	-3.731	0.213	1.00	30.62

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478	O	ALA	A	179	31.466	-3.697	0.192	1.00	30.86
479	CB	ALA	A	179	33.856	-3.733	2.401	1.00	34.25
480	N	ASN	A	180	33.420	-2.907	-0.561	1.00	29.04
481	CA	ASN	A	180	32.851	-2.015	-1.558	1.00	28.58
482	C	ASN	A	180	33.499	-2.211	-2.939	1.00	27.39
483	O	ASN	A	180	34.638	-2.689	-3.042	1.00	26.95
484	CB	ASN	A	180	32.957	-0.521	-1.148	1.00	29.90
485	CG	ASN	A	180	32.103	-0.258	0.104	1.00	31.68
486	OD1	ASN	A	180	30.885	-0.552	0.100	1.00	34.34
487	ND2	ASN	A	180	32.750	0.063	1.209	1.00	32.41
488	N	ASN	A	181	32.825	-1.832	-4.017	1.00	25.75
489	CA	ASN	A	181	33.370	-1.875	-5.372	1.00	25.22
490	C	ASN	A	181	34.287	-0.683	-5.625	1.00	24.74
491	O	ASN	A	181	34.253	0.299	-4.849	1.00	23.10
492	CB	ASN	A	181	32.221	-1.881	-6.393	1.00	24.36
493	CG	ASN	A	181	31.526	-3.216	-6.503	1.00	23.81
494	OD1	ASN	A	181	30.312	-3.231	-6.776	1.00	25.93
495	ND2	ASN	A	181	32.208	-4.326	-6.339	1.00	19.94
496	N	TRP	A	182	35.132	-0.743	-6.657	1.00	23.37
497	CA	TRP	A	182	36.096	0.317	-6.986	1.00	22.89
498	C	TRP	A	182	36.812	0.884	-5.748	1.00	24.90
499	O	TRP	A	182	36.686	2.061	-5.356	1.00	22.19
500	CB	TRP	A	182	35.440	1.390	-7.842	1.00	21.88
501	CG	TRP	A	182	34.968	0.888	-9.213	1.00	21.19
502	CD1	TRP	A	182	33.661	0.662	-9.556	1.00	20.22
503	CD2	TRP	A	182	35.772	0.587	-10.354	1.00	20.33
504	NE1	TRP	A	182	33.620	0.238	-10.890	1.00	21.14
505	CE2	TRP	A	182	34.899	0.206	-11.396	1.00	20.92
506	CE3	TRP	A	182	37.140	0.646	-10.652	1.00	19.83
507	CZ2	TRP	A	182	35.335	-0.126	-12.679	1.00	19.37
508	CZ3	TRP	A	182	37.588	0.290	-11.911	1.00	20.08
509	CH2	TRP	A	182	36.682	-0.111	-12.925	1.00	18.62
510	N	SER	A	183	37.553	-0.028	-5.091	1.00	24.20
511	CA	SER	A	183	38.166	0.298	-3.787	1.00	25.99
512	C	SER	A	183	39.619	-0.056	-3.755	1.00	25.00
513	O	SER	A	183	40.038	-1.222	-3.552	1.00	24.72
514	CB	SER	A	183	37.250	-0.396	-2.744	1.00	27.68
515	OG	SER	A	183	37.806	-0.303	-1.422	1.00	31.94
516	N	PRO	A	184	40.504	0.901	-3.999	1.00	24.27
517	CA	PRO	A	184	41.936	0.660	-4.076	1.00	25.54
518	C	PRO	A	184	42.583	0.218	-2.771	1.00	27.63
519	O	PRO	A	184	43.702	-0.312	-2.819	1.00	26.74
520	CB	PRO	A	184	42.567	2.002	-4.480	1.00	25.19
521	CG	PRO	A	184	41.436	2.850	-4.939	1.00	27.00
522	CD	PRO	A	184	40.171	2.317	-4.293	1.00	25.48
523	N	ASP	A	185	41.953	0.501	-1.660	1.00	28.67
524	CA	ASP	A	185	42.469	0.243	-0.330	1.00	35.01
525	C	ASP	A	185	42.168	-1.154	0.186	1.00	32.77
526	O	ASP	A	185	42.631	-1.481	1.276	1.00	32.78
527	CB	ASP	A	185	41.794	1.331	0.575	1.00	40.22
528	CG	ASP	A	185	40.328	0.971	0.823	1.00	45.75
529	OD1	ASP	A	185	39.796	-0.145	0.631	1.00	49.67
530	OD2	ASP	A	185	39.665	1.968	1.250	1.00	48.92
531	N	ASP	A	186	41.216	-1.836	-0.471	1.00	30.11
532	CA	ASP	A	186	40.727	-3.109	0.072	1.00	29.50
533	C	ASP	A	186	41.595	-4.279	-0.355	1.00	28.84
534	O	ASP	A	186	41.578	-4.767	-1.473	1.00	26.82
535	CB	ASP	A	186	39.253	-3.271	-0.280	1.00	29.89
536	CG	ASP	A	186	38.521	-4.309	0.548	1.00	30.33
537	OD1	ASP	A	186	39.135	-5.357	0.847	1.00	30.32
538	OD2	ASP	A	186	37.337	-4.120	0.897	1.00	29.44
539	N	ASP	A	187	42.390	-4.757	0.617	1.00	28.04
540	CA	ASP	A	187	43.314	-5.849	0.376	1.00	28.05
541	C	ASP	A	187	42.680	-7.218	0.204	1.00	26.64
542	O	ASP	A	187	43.469	-8.146	0.051	1.00	26.92
543	CB	ASP	A	187	44.447	-5.977	1.403	1.00	29.12
544	CG	ASP	A	187	45.562	-5.006	1.075	1.00	29.66
545	OD1	ASP	A	187	45.560	-4.414	-0.035	1.00	29.31
546	OD2	ASP	A	187	46.419	-4.719	1.940	1.00	30.32
547	N	HIS	A	188	41.382	-7.380	0.101	1.00	25.81
548	CA	HIS	A	188	40.750	-8.635	-0.234	1.00	28.57
549	C	HIS	A	188	41.034	-8.980	-1.719	1.00	28.04
550	O	HIS	A	188	40.988	-10.162	-2.051	1.00	25.11
551	CB	HIS	A	188	39.247	-8.622	0.001	1.00	31.30
552	CG	HIS	A	188	38.773	-8.598	1.420	1.00	35.25
553	ND1	HIS	A	188	38.178	-9.695	2.019	1.00	36.56
554	CD2	HIS	A	188	38.785	-7.621	2.366	1.00	36.05
555	CE1	HIS	A	188	37.843	-9.392	3.263	1.00	37.12
556	NE2	HIS	A	188	38.209	-8.137	3.496	1.00	38.08
557	N	THR	A	189	41.419	-8.003	-2.549	1.00	25.78
558	CA	THR	A	189	41.749	-8.277	-3.944	1.00	25.63
559	C	THR	A	189	43.164	-7.831	-4.295	1.00	26.53
560	O	THR	A	189	43.525	-7.508	-5.446	1.00	25.53
561	CB	THR	A	189	40.736	-7.696	-4.945	1.00	24.83
562	OG1	THR	A	189	40.551	-6.312	-4.648	1.00	23.22
563	CG2	THR	A	189	39.397	-8.428	-4.913	1.00	24.10
564	N	LEU	A	190	44.036	-7.871	-3.278	1.00	24.47
565	CA	LEU	A	190	45.446	-7.592	-3.497	1.00	25.02
566	C	LEU	A	190	46.106	-8.740	-4.276	1.00	25.66
567	O	LEU	A	190	45.947	-9.871	-3.821	1.00	24.54
568	CB	LEU	A	190	46.115	-7.493	-2.126	1.00	25.49
569	CG	LEU	A	190	47.612	-7.221	-2.066	1.00	26.63
570	CD1	LEU	A	190	47.961	-5.811	-2.561	1.00	26.87
571	CD2	LEU	A	190	48.107	-7.483	-0.649	1.00	26.92
572	N	LEU	A	191	46.785	-8.501	-5.397	1.00	23.25
573	CA	LEU	A	191	47.424	-9.589	-6.120	1.00	22.73

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574	C	LEU	A	191	48.627	-10.118	-5.353	1.00	23.44
575	O	LEU	A	191	49.390	-9.351	-4.748	1.00	21.57
576	CB	LEU	A	191	47.921	-9.125	-7.510	1.00	21.62
577	CG	LEU	A	191	46.880	-8.960	-8.614	1.00	21.93
578	CD1	LEU	A	191	45.698	-8.077	-8.268	1.00	18.64
579	CD2	LEU	A	191	47.599	-8.457	-9.886	1.00	21.63
580	N	LYS	A	192	48.898	-11.403	-5.497	1.00	23.59
581	CA	LYS	A	192	50.006	-12.052	-4.827	1.00	24.86
582	C	LYS	A	192	51.232	-12.227	-5.700	1.00	26.50
583	O	LYS	A	192	51.100	-12.428	-6.912	1.00	26.86
584	CB	LYS	A	192	49.560	-13.491	-4.421	1.00	25.31
585	CG	LYS	A	192	48.449	-13.455	-3.375	1.00	27.13
586	CD	LYS	A	192	47.815	-14.750	-3.079	0.00	20.00
587	CE	LYS	A	192	46.420	-14.700	-2.448	0.00	20.00
588	NZ	LYS	A	192	46.039	-16.034	-1.988	0.00	20.00
589	N	LYS	A	193	52.413	-12.326	-5.098	1.00	27.68
590	CA	LYS	A	193	53.593	-12.532	-5.943	1.00	32.22
591	C	LYS	A	193	53.825	-13.987	-6.288	1.00	32.50
592	O	LYS	A	193	53.939	-14.822	-5.409	1.00	30.76
593	CB	LYS	A	193	54.734	-11.805	-5.260	1.00	35.25
594	CG	LYS	A	193	56.021	-12.513	-4.979	1.00	39.64
595	CD	LYS	A	193	57.217	-11.595	-5.033	1.00	41.28
596	CE	LYS	A	193	58.106	-11.653	-3.808	1.00	44.51
597	NZ	LYS	A	193	59.154	-10.583	-3.791	1.00	45.93
598	N	ILE	A	194	53.836	-14.305	-7.593	1.00	30.97
599	CA	ILE	A	194	54.161	-15.631	-8.117	1.00	29.28
600	C	ILE	A	194	55.654	-15.716	-8.412	1.00	28.94
601	O	ILE	A	194	56.334	-16.725	-8.177	1.00	28.26
602	CB	ILE	A	194	53.341	-15.917	-9.394	1.00	30.80
603	CG1	ILE	A	194	51.872	-15.560	-9.172	1.00	29.46
604	CG2	ILE	A	194	53.505	-17.363	-9.869	1.00	30.31
605	CD1	ILE	A	194	51.129	-16.279	-8.076	1.00	29.66
606	N	ASN	A	195	56.246	-14.658	-8.969	1.00	26.41
607	CA	ASN	A	195	57.689	-14.582	-9.209	1.00	25.15
608	C	ASN	A	195	57.982	-13.108	-9.056	1.00	25.32
609	O	ASN	A	195	57.060	-12.285	-9.010	1.00	24.84
610	CB	ASN	A	195	58.205	-15.255	-10.468	1.00	26.01
611	CG	ASN	A	195	58.002	-14.588	-11.816	1.00	23.49
612	OD1	ASN	A	195	58.324	-13.419	-11.979	1.00	22.62
613	ND2	ASN	A	195	57.463	-15.271	-12.821	1.00	21.61
614	N	PRO	A	196	59.222	-12.681	-8.921	1.00	27.18
615	CA	PRO	A	196	59.566	-11.282	-8.695	1.00	27.81
616	C	PRO	A	196	59.014	-10.304	-9.712	1.00	28.82
617	O	PRO	A	196	58.874	-9.118	-9.403	1.00	29.64
618	CB	PRO	A	196	61.088	-11.245	-8.660	1.00	27.55
619	CG	PRO	A	196	61.562	-12.641	-8.735	1.00	27.99
620	CD	PRO	A	196	60.400	-13.571	-8.910	1.00	27.24
621	N	ASN	A	197	58.728	-10.737	-10.939	1.00	28.40
622	CA	ASN	A	197	58.152	-9.868	-11.964	1.00	27.61
623	C	ASN	A	197	56.808	-10.412	-12.426	1.00	26.54
624	O	ASN	A	197	56.446	-10.216	-13.588	1.00	24.74
625	CB	ASN	A	197	59.156	-9.685	-13.114	1.00	25.82
626	CG	ASN	A	197	58.874	-8.553	-14.073	1.00	24.90
627	OD1	ASN	A	197	58.401	-7.487	-13.679	1.00	25.87
628	ND2	ASN	A	197	59.143	-8.694	-15.374	1.00	22.51
629	N	LEU	A	198	56.003	-11.008	-11.527	1.00	25.03
630	CA	LEU	A	198	54.709	-11.567	-11.921	1.00	25.50
631	C	LEU	A	198	53.734	-11.604	-10.757	1.00	24.75
632	O	LEU	A	198	54.037	-12.353	-9.805	1.00	24.83
633	CB	LEU	A	198	54.639	-12.947	-12.600	1.00	26.19
634	CG	LEU	A	198	53.385	-13.711	-13.032	1.00	29.17
635	CD1	LEU	A	198	52.653	-13.174	-14.263	1.00	28.46
636	CD2	LEU	A	198	54.064	-15.009	-13.469	1.00	31.33
637	N	TYR	A	199	52.635	-10.883	-10.781	1.00	22.56
638	CA	TYR	A	199	51.640	-10.794	-9.724	1.00	22.64
639	C	TYR	A	199	50.281	-11.275	-10.192	1.00	23.37
640	O	TYR	A	199	49.898	-10.900	-11.326	1.00	21.85
641	CB	TYR	A	199	51.488	-9.332	-9.172	1.00	22.41
642	CG	TYR	A	199	52.673	-9.037	-8.251	1.00	24.19
643	CD1	TYR	A	199	52.525	-9.019	-6.870	1.00	24.33
644	CD2	TYR	A	199	53.955	-8.856	-8.753	1.00	24.63
645	CE1	TYR	A	199	53.599	-8.782	-6.021	1.00	23.22
646	CE2	TYR	A	199	55.047	-8.650	-7.934	1.00	24.30
647	CZ	TYR	A	199	54.848	-8.607	-6.552	1.00	25.35
648	OH	TYR	A	199	55.967	-8.424	-5.758	1.00	25.36
649	N	GLN	A	200	49.593	-12.153	-9.437	1.00	21.46
650	CA	GLN	A	200	48.319	-12.703	-9.851	1.00	22.78
651	C	GLN	A	200	47.308	-12.901	-8.709	1.00	23.92
652	O	GLN	A	200	47.642	-12.965	-7.529	1.00	23.20
653	CB	GLN	A	200	48.460	-14.071	-10.554	1.00	23.72
654	CG	GLN	A	200	49.326	-14.123	-11.818	1.00	23.30
655	CD	GLN	A	200	49.357	-15.468	-12.509	1.00	24.08
656	OE1	GLN	A	200	48.907	-15.563	-13.665	1.00	25.79
657	NE2	GLN	A	200	49.802	-16.529	-11.838	1.00	21.68
658	N	LEU	A	201	46.029	-12.854	-9.068	1.00	22.79
659	CA	LEU	A	201	44.878	-13.063	-8.223	1.00	23.86
660	C	LEU	A	201	43.871	-13.926	-8.993	1.00	22.76
661	O	LEU	A	201	43.615	-13.595	-10.149	1.00	20.39
662	CB	LEU	A	201	44.180	-11.770	-7.798	1.00	24.31
663	CG	LEU	A	201	42.984	-11.871	-6.855	1.00	27.82
664	CD1	LEU	A	201	43.423	-12.292	-5.451	1.00	28.00
665	CD2	LEU	A	201	42.247	-10.531	-6.725	1.00	26.81
666	N	SER	A	202	43.269	-14.938	-8.367	1.00	21.06
667	CA	SER	A	202	42.217	-15.727	-8.956	1.00	20.94
668	C	SER	A	202	40.969	-15.724	-8.085	1.00	24.18
669	O	SER	A	202	41.140	-15.747	-6.843	1.00	26.01

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670	CB	SER	A	202	42.700	-17.198	-9.057	1.00	21.57
671	OG	SER	A	202	43.669	-17.342	-10.101	1.00	24.54
672	N	GLY	A	203	39.768	-15.823	-8.623	1.00	24.80
673	CA	GLY	A	203	38.565	-15.892	-7.834	1.00	25.89
674	C	GLY	A	203	37.359	-16.159	-8.711	1.00	28.12
675	O	GLY	A	203	37.385	-15.914	-9.919	1.00	28.11
676	N	THR	A	204	36.305	-16.716	-8.088	1.00	27.74
677	CA	THR	A	204	35.097	-17.110	-8.779	1.00	26.86
678	C	THR	A	204	34.105	-15.971	-8.927	1.00	26.50
679	O	THR	A	204	33.813	-15.312	-7.936	1.00	26.91
680	CB	THR	A	204	34.383	-18.207	-7.933	1.00	29.21
681	OG1	THR	A	204	35.262	-19.322	-7.816	1.00	28.46
682	CG2	THR	A	204	33.059	-18.617	-8.581	1.00	28.38
683	N	LEU	A	205	33.575	-15.738	-10.119	1.00	25.28
684	CA	LEU	A	205	32.594	-14.705	-10.324	1.00	27.14
685	C	LEU	A	205	31.303	-15.289	-10.898	1.00	29.05
686	O	LEU	A	205	31.325	-16.121	-11.802	1.00	27.54
687	CB	LEU	A	205	33.139	-13.666	-11.307	1.00	27.39
688	CG	LEU	A	205	34.340	-12.803	-10.896	1.00	27.95
689	CD1	LEU	A	205	34.858	-12.022	-12.101	1.00	27.28
690	CD2	LEU	A	205	33.999	-11.861	-9.743	1.00	29.19
691	N	PRO	A	206	30.154	-14.795	-10.441	1.00	30.40
692	CA	PRO	A	206	28.870	-15.199	-11.005	1.00	30.93
693	C	PRO	A	206	28.882	-14.794	-12.473	1.00	31.99
694	O	PRO	A	206	29.702	-13.916	-12.809	1.00	32.25
695	CB	PRO	A	206	27.830	-14.370	-10.241	1.00	30.06
696	CG	PRO	A	206	28.518	-13.896	-9.020	1.00	30.95
697	CD	PRO	A	206	30.006	-13.818	-9.345	1.00	31.23
698	N	ALA	A	207	27.959	-15.236	-13.292	1.00	30.94
699	CA	ALA	A	207	27.829	-14.752	-14.647	1.00	32.79
700	C	ALA	A	207	27.525	-13.250	-14.646	1.00	33.93
701	O	ALA	A	207	26.875	-12.784	-13.698	1.00	33.84
702	CB	ALA	A	207	26.644	-15.405	-15.344	1.00	33.37
703	N	GLY	A	208	27.891	-12.554	-15.717	1.00	33.30
704	CA	GLY	A	208	27.627	-11.117	-15.815	1.00	33.40
705	C	GLY	A	208	28.764	-10.431	-16.590	1.00	34.81
706	O	GLY	A	208	29.748	-11.089	-16.954	1.00	34.75
707	N	THR	A	209	28.631	-9.147	-16.855	1.00	33.68
708	CA	THR	A	209	29.649	-8.364	-17.553	1.00	35.01
709	C	THR	A	209	30.168	-7.337	-16.549	1.00	32.85
710	O	THR	A	209	29.371	-6.687	-15.843	1.00	31.81
711	CB	THR	A	209	29.126	-7.714	-18.837	1.00	37.54
712	OG1	THR	A	209	30.036	-6.711	-19.353	1.00	40.79
713	CG2	THR	A	209	27.808	-7.044	-18.521	1.00	38.82
714	N	TYR	A	210	31.475	-7.356	-16.327	1.00	28.47
715	CA	TYR	A	210	32.119	-6.499	-15.331	1.00	25.61
716	C	TYR	A	210	33.148	-5.574	-15.968	1.00	23.20
717	O	TYR	A	210	33.511	-5.730	-17.129	1.00	20.43
718	CB	TYR	A	210	32.853	-7.361	-14.285	1.00	25.13
719	CG	TYR	A	210	32.043	-8.437	-13.604	1.00	25.77
720	CD1	TYR	A	210	31.418	-8.187	-12.385	1.00	26.19
721	CD2	TYR	A	210	31.878	-9.699	-14.159	1.00	26.65
722	CE1	TYR	A	210	30.647	-9.141	-11.755	1.00	25.94
723	CE2	TYR	A	210	31.129	-10.686	-13.531	1.00	26.59
724	CZ	TYR	A	210	30.508	-10.392	-12.330	1.00	27.30
725	OH	TYR	A	210	29.776	-11.352	-11.675	1.00	28.27
726	N	GLN	A	211	33.707	-4.664	-15.180	1.00	21.51
727	CA	GLN	A	211	34.770	-3.769	-15.611	1.00	21.91
728	C	GLN	A	211	35.851	-3.700	-14.517	1.00	20.11
729	O	GLN	A	211	35.444	-3.737	-13.367	1.00	19.22
730	CB	GLN	A	211	34.270	-2.358	-15.949	1.00	20.26
731	CG	GLN	A	211	33.515	-2.252	-17.274	1.00	21.03
732	CD	GLN	A	211	32.948	-0.889	-17.595	1.00	21.84
733	OE1	GLN	A	211	32.192	-0.698	-18.590	1.00	23.95
734	NE2	GLN	A	211	33.387	0.136	-16.876	1.00	20.75
735	N	TYR	A	212	37.144	-3.613	-14.861	1.00	18.80
736	CA	TYR	A	212	38.126	-3.616	-13.782	1.00	19.43
737	C	TYR	A	212	39.418	-2.932	-14.206	1.00	20.03
738	O	TYR	A	212	39.722	-2.780	-15.384	1.00	17.17
739	CB	TYR	A	212	38.434	-5.067	-13.433	1.00	20.14
740	CG	TYR	A	212	39.327	-5.644	-14.475	1.00	20.47
741	CD1	TYR	A	212	38.790	-6.478	-15.451	1.00	19.52
742	CD2	TYR	A	212	40.715	-5.503	-14.382	1.00	19.82
743	CE1	TYR	A	212	39.622	-7.192	-16.297	1.00	18.82
744	CE2	TYR	A	212	41.549	-6.216	-15.233	1.00	20.89
745	CZ	TYR	A	212	41.006	-7.061	-16.184	1.00	19.83
746	OH	TYR	A	212	41.824	-7.773	-17.038	1.00	20.51
747	N	LYS	A	213	40.166	-2.472	-13.189	1.00	18.54
748	CA	LYS	A	213	41.504	-1.960	-13.442	1.00	19.62
749	C	LYS	A	213	42.481	-2.457	-12.374	1.00	19.10
750	O	LYS	A	213	42.131	-3.179	-11.451	1.00	21.19
751	CB	LYS	A	213	41.449	-0.429	-13.444	1.00	20.40
752	CG	LYS	A	213	40.902	0.131	-14.757	1.00	19.33
753	CD	LYS	A	213	41.325	1.584	-14.995	1.00	21.89
754	CE	LYS	A	213	40.838	2.532	-13.895	1.00	24.44
755	NZ	LYS	A	213	41.231	3.905	-14.220	1.00	26.58
756	N	ILE	A	214	43.762	-2.212	-12.362	1.00	18.54
757	CA	ILE	A	214	44.727	-2.502	-11.342	1.00	19.13
758	C	ILE	A	214	45.225	-1.142	-10.779	1.00	20.65
759	O	ILE	A	214	45.930	-0.422	-11.489	1.00	17.06
760	CB	ILE	A	214	45.969	-3.255	-11.847	1.00	19.87
761	CG1	ILE	A	214	45.679	-4.554	-12.610	1.00	20.30
762	CG2	ILE	A	214	46.957	-3.514	-10.703	1.00	18.99
763	CD1	ILE	A	214	44.772	-5.587	-11.986	1.00	19.54
764	N	ALA	A	215	44.970	-0.894	-9.489	1.00	21.29
765	CA	ALA	A	215	45.406	0.360	-8.837	1.00	21.91

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766	C	ALA	A	215	46.590	0.082	-7.923	1.00	22.37
767	O	ALA	A	215	46.588	-0.953	-7.226	1.00	21.58
768	CB	ALA	A	215	44.222	0.911	-7.989	1.00	20.97
769	N	LEU	A	216	47.641	0.873	-7.988	1.00	21.99
770	CA	LEU	A	216	48.845	0.752	-7.159	1.00	22.55
771	C	LEU	A	216	48.759	1.510	-5.817	1.00	24.71
772	O	LEU	A	216	48.006	2.458	-5.641	1.00	22.08
773	CB	LEU	A	216	50.029	1.290	-7.964	1.00	23.76
774	CG	LEU	A	216	50.319	0.462	-9.216	1.00	22.14
775	CD1	LEU	A	216	51.686	0.786	-9.825	1.00	22.16
776	CD2	LEU	A	216	50.316	-1.042	-8.946	1.00	24.20
777	N	ASP	A	217	49.548	1.000	-4.839	1.00	24.74
778	CA	ASP	A	217	49.861	1.748	-3.610	1.00	28.00
779	C	ASP	A	217	48.639	2.264	-2.839	1.00	29.70
780	O	ASP	A	217	48.678	3.296	-2.182	1.00	30.51
781	CB	ASP	A	217	50.783	2.907	-3.980	1.00	27.70
782	CG	ASP	A	217	52.039	2.351	-4.632	1.00	28.23
783	OD1	ASP	A	217	52.497	1.300	-4.187	1.00	25.51
784	OD2	ASP	A	217	52.537	2.962	-5.574	1.00	29.46
785	N	HIS	A	218	47.515	1.528	-2.878	1.00	28.93
786	CA	HIS	A	218	46.336	1.913	-2.179	1.00	31.04
787	C	HIS	A	218	45.820	3.308	-2.512	1.00	32.01
788	O	HIS	A	218	45.314	3.968	-1.594	1.00	33.76
789	CB	HIS	A	218	46.580	1.848	-0.656	1.00	32.62
790	CG	HIS	A	218	46.763	0.494	-0.095	1.00	34.70
791	ND1	HIS	A	218	46.289	-0.669	-0.712	1.00	35.05
792	CD2	HIS	A	218	47.351	0.031	1.035	1.00	36.61
793	CE1	HIS	A	218	46.572	-1.745	-0.006	1.00	35.70
794	NE2	HIS	A	218	47.230	-1.346	1.068	1.00	38.00
795	N	SER	A	219	45.873	3.742	-3.746	1.00	30.50
796	CA	SER	A	219	45.437	5.088	-4.114	1.00	29.81
797	C	SER	A	219	44.927	5.097	-5.553	1.00	28.38
798	O	SER	A	219	45.236	4.171	-6.317	1.00	26.48
799	CB	SER	A	219	46.673	5.978	-3.940	1.00	31.74
800	OG	SER	A	219	46.686	7.146	-4.725	1.00	33.53
801	N	TRP	A	220	44.295	6.201	-5.943	1.00	26.47
802	CA	TRP	A	220	43.880	6.481	-7.293	1.00	27.86
803	C	TRP	A	220	44.969	7.170	-8.118	1.00	28.10
804	O	TRP	A	220	44.749	7.371	-9.326	1.00	27.08
805	CB	TRP	A	220	42.620	7.353	-7.351	1.00	28.03
806	CG	TRP	A	220	41.346	6.631	-7.044	1.00	27.68
807	CD1	TRP	A	220	40.441	6.925	-6.071	1.00	26.78
808	CD2	TRP	A	220	40.843	5.467	-7.730	1.00	26.84
809	NE1	TRP	A	220	39.395	6.022	-6.110	1.00	27.04
810	CE2	TRP	A	220	39.632	5.109	-7.121	1.00	26.56
811	CE3	TRP	A	220	41.320	4.690	-8.788	1.00	27.09
812	CZ2	TRP	A	220	38.876	4.018	-7.520	1.00	25.18
813	CZ3	TRP	A	220	40.583	3.615	-9.210	1.00	26.81
814	CH2	TRP	A	220	39.369	3.287	-8.557	1.00	26.52
815	N	ASN	A	221	46.109	7.509	-7.535	1.00	27.91
816	CA	ASN	A	221	47.167	8.184	-8.277	1.00	29.33
817	C	ASN	A	221	47.613	7.441	-9.528	1.00	29.98
818	O	ASN	A	221	47.834	8.056	-10.580	1.00	29.96
819	CB	ASN	A	221	48.384	8.377	-7.354	1.00	32.21
820	CG	ASN	A	221	48.207	9.429	-6.270	1.00	35.96
821	OD1	ASN	A	221	47.216	10.178	-6.276	1.00	39.36
822	ND2	ASN	A	221	49.141	9.546	-5.324	1.00	35.91
823	N	THR	A	222	47.864	6.135	-9.421	1.00	28.62
824	CA	THR	A	222	48.373	5.326	-10.511	1.00	27.05
825	C	THR	A	222	47.570	4.034	-10.661	1.00	25.67
826	O	THR	A	222	47.542	3.226	-9.734	1.00	22.27
827	CB	THR	A	222	49.869	5.008	-10.320	1.00	28.65
828	OG1	THR	A	222	50.605	6.252	-10.393	1.00	30.47
829	CG2	THR	A	222	50.488	4.129	-11.413	1.00	28.53
830	N	SER	A	223	47.016	3.848	-11.867	1.00	23.93
831	CA	SER	A	223	46.277	2.629	-12.199	1.00	22.41
832	C	SER	A	223	46.504	2.179	-13.656	1.00	22.11
833	O	SER	A	223	46.870	3.009	-14.521	1.00	20.61
834	CB	SER	A	223	44.791	2.770	-11.925	1.00	21.37
835	OG	SER	A	223	44.098	3.680	-12.748	1.00	21.13
836	N	TYR	A	224	46.306	0.904	-13.924	1.00	19.54
837	CA	TYR	A	224	46.392	0.447	-15.308	1.00	20.33
838	C	TYR	A	224	45.256	-0.515	-15.656	1.00	23.40
839	O	TYR	A	224	44.678	-1.178	-14.806	1.00	21.40
840	CB	TYR	A	224	47.730	-0.269	-15.496	1.00	20.56
841	CG	TYR	A	224	48.851	0.617	-15.090	1.00	20.58
842	CD1	TYR	A	224	49.428	0.464	-13.833	1.00	21.98
843	CD2	TYR	A	224	49.429	1.488	-16.013	1.00	22.63
844	CE1	TYR	A	224	50.382	1.159	-13.505	1.00	22.51
845	CE2	TYR	A	224	50.581	2.186	-15.685	1.00	23.45
846	CZ	TYR	A	224	51.161	2.018	-14.440	1.00	23.93
847	OH	TYR	A	224	52.340	2.665	-14.126	1.00	26.78
848	N	PRO	A	225	44.910	-0.545	-16.957	1.00	23.50
849	CA	PRO	A	225	45.501	0.350	-17.935	1.00	22.64
850	C	PRO	A	225	44.900	1.756	-17.867	1.00	22.45
851	O	PRO	A	225	44.313	2.161	-18.872	1.00	21.99
852	CB	PRO	A	225	45.385	-0.335	-19.294	1.00	23.11
853	CG	PRO	A	225	44.382	-1.484	-19.173	1.00	23.73
854	CD	PRO	A	225	43.979	-1.435	-17.622	1.00	22.80
855	N	GLY	A	226	45.077	2.458	-19.001	1.00	21.76
856	CA	GLY	A	226	44.559	3.812	-19.040	1.00	21.93
857	C	GLY	A	226	43.022	3.923	-19.125	1.00	23.76
858	O	GLY	A	226	42.405	4.932	-18.809	1.00	23.80
859	N	ASN	A	227	42.466	2.802	-19.616	1.00	23.49
860	CA	ASN	A	227	41.018	2.737	-19.670	1.00	24.79
861	C	ASN	A	227	40.364	1.416	-18.959	1.00	23.66

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862	O	ASN	A	227	41.160	0.489	-18.779	1.00	21.15
863	CB	ASN	A	227	40.210	2.594	-21.106	1.00	26.98
864	CG	ASN	A	227	40.485	3.892	-21.877	1.00	29.55
865	OD1	ASN	A	227	40.418	4.994	-21.332	1.00	31.48
866	ND2	ASN	A	227	40.823	3.724	-23.148	1.00	31.22
867	N	ASN	A	228	39.094	1.377	-18.571	1.00	23.20
868	CA	ASN	A	228	38.573	0.197	-17.841	1.00	22.62
869	C	ASN	A	228	38.683	-1.049	-18.724	1.00	22.14
870	O	ASN	A	228	38.483	-0.972	-19.949	1.00	21.31
871	CB	ASN	A	228	37.100	0.435	-17.487	1.00	21.69
872	CG	ASN	A	228	36.803	1.486	-16.423	1.00	21.12
873	OD1	ASN	A	228	35.598	1.769	-16.125	1.00	21.53
874	ND2	ASN	A	228	37.794	2.076	-15.831	1.00	18.06
875	N	VAL	A	229	38.857	-2.232	-18.162	1.00	22.54
876	CA	VAL	A	229	38.894	-3.464	-18.981	1.00	20.25
877	C	VAL	A	229	37.524	-4.125	-18.851	1.00	20.80
878	O	VAL	A	229	37.078	-4.359	-17.734	1.00	20.94
879	CB	VAL	A	229	39.990	-4.473	-18.584	1.00	19.95
880	CG1	VAL	A	229	39.902	-5.771	-19.415	1.00	14.74
881	CG2	VAL	A	229	41.389	-3.855	-18.689	1.00	15.89
882	N	SER	A	230	36.894	-4.469	-19.964	1.00	21.31
883	CA	SER	A	230	35.595	-5.158	-19.969	1.00	22.94
884	C	SER	A	230	35.778	-6.674	-19.896	1.00	24.31
885	O	SER	A	230	36.593	-7.269	-20.616	1.00	21.95
886	CB	SER	A	230	34.819	-4.769	-21.221	1.00	24.67
887	OG	SER	A	230	33.548	-5.431	-21.269	1.00	28.19
888	N	LEU	A	231	35.049	-7.328	-18.993	1.00	24.99
889	CA	LEU	A	231	35.108	-8.754	-18.760	1.00	26.33
890	C	LEU	A	231	33.709	-9.391	-18.724	1.00	29.37
891	O	LEU	A	231	32.966	-9.135	-17.764	1.00	28.67
892	CB	LEU	A	231	35.779	-9.047	-17.422	1.00	25.50
893	CG	LEU	A	231	35.801	-10.449	-16.823	1.00	26.01
894	CD1	LEU	A	231	36.671	-11.424	-17.607	1.00	25.54
895	CD2	LEU	A	231	36.348	-10.425	-15.384	1.00	25.86
896	N	THR	A	232	33.400	-10.266	-19.692	1.00	30.00
897	CA	THR	A	232	32.070	-10.894	-19.612	1.00	32.54
898	C	THR	A	232	32.246	-12.342	-19.188	1.00	32.86
899	O	THR	A	232	33.069	-13.072	-19.750	1.00	32.67
900	CB	THR	A	232	31.143	-10.753	-20.806	1.00	33.54
901	OG1	THR	A	232	31.043	-11.964	-21.567	1.00	37.56
902	CG2	THR	A	232	31.478	-9.607	-21.734	1.00	30.68
903	N	VAL	A	233	31.540	-12.713	-18.135	1.00	33.79
904	CA	VAL	A	233	31.579	-14.068	-17.613	1.00	36.22
905	C	VAL	A	233	30.298	-14.809	-17.947	1.00	38.71
906	O	VAL	A	233	29.186	-14.331	-17.740	1.00	37.77
907	CB	VAL	A	233	31.792	-13.955	-16.105	1.00	35.04
908	CG1	VAL	A	233	31.838	-15.338	-15.489	1.00	35.88
909	CG2	VAL	A	233	33.107	-13.252	-15.847	1.00	33.72
910	N	PRO	A	234	30.486	-16.031	-18.513	1.00	41.11
911	CA	PRO	A	234	29.393	-16.841	-19.027	1.00	42.50
912	C	PRO	A	234	28.491	-17.443	-17.947	1.00	43.33
913	O	PRO	A	234	28.940	-17.865	-16.889	1.00	45.44
914	CB	PRO	A	234	29.993	-18.031	-19.783	1.00	41.71
915	CG	PRO	A	234	31.509	-17.862	-19.793	1.00	42.81
916	CD	PRO	A	234	31.725	-16.769	-18.640	1.00	42.19
917	N	GLN	A	235	27.199	-17.504	-18.314	1.00	20.00
918	CA	GLN	A	235	26.246	-18.000	-17.341	1.00	20.00
919	C	GLN	A	235	26.543	-19.290	-16.567	1.00	20.00
920	O	GLN	A	235	26.691	-20.364	-17.135	1.00	20.00
921	CB	GLN	A	235	24.891	-18.189	-18.091	0.00	20.00
922	CG	GLN	A	235	23.744	-18.642	-17.182	0.00	20.00
923	CD	GLN	A	235	22.488	-18.822	-18.002	0.00	20.00
924	OE1	GLN	A	235	21.427	-19.185	-17.522	0.00	20.00
925	NE2	GLN	A	235	22.653	-18.554	-19.313	0.00	20.00
926	N	GLY	A	236	26.571	-19.113	-15.235	1.00	20.00
927	CA	GLY	A	236	26.914	-20.255	-14.411	1.00	20.00
928	C	GLY	A	236	28.215	-19.843	-13.723	1.00	20.00
929	O	GLY	A	236	28.571	-20.322	-12.660	1.00	20.00
930	N	GLY	A	237	28.951	-18.960	-14.432	1.00	45.11
931	CA	GLY	A	237	30.099	-18.275	-13.853	1.00	43.81
932	C	GLY	A	237	31.386	-19.060	-14.065	1.00	41.23
933	O	GLY	A	237	31.412	-20.077	-14.716	1.00	41.47
934	N	GLU	A	238	32.494	-18.495	-13.570	1.00	39.53
935	CA	GLU	A	238	33.738	-19.269	-13.544	1.00	36.93
936	C	GLU	A	238	34.814	-18.623	-12.658	1.00	35.69
937	O	GLU	A	238	34.687	-17.510	-12.178	1.00	34.73
938	CB	GLU	A	238	34.249	-19.376	-14.974	1.00	37.46
939	CG	GLU	A	238	34.152	-18.042	-15.715	1.00	38.60
940	CD	GLU	A	238	34.928	-18.141	-17.002	1.00	38.06
941	OE1	GLU	A	238	36.045	-17.645	-17.053	1.00	39.51
942	OE2	GLU	A	238	34.397	-18.708	-17.948	1.00	39.63
943	N	LYS	A	239	35.917	-19.366	-12.434	1.00	31.34
944	CA	LYS	A	239	36.752	-18.708	-12.071	1.00	30.50
945	C	LYS	A	239	38.005	-18.078	-12.734	1.00	29.49
946	O	LYS	A	239	38.644	-18.729	-13.541	1.00	26.10
947	CB	LYS	A	239	37.649	-19.635	-11.230	1.00	30.57
948	CG	LYS	A	239	39.081	-19.338	-10.780	1.00	32.75
949	CD	LYS	A	239	39.203	-19.871	-9.351	1.00	35.35
950	CE	LYS	A	239	39.279	-21.314	-8.840	1.00	36.50
951	NZ	LYS	A	239	39.762	-21.354	-7.461	1.00	33.54
952	N	VAL	A	240	38.248	-16.787	-12.495	1.00	26.95
953	CA	VAL	A	240	39.095	-15.992	-13.399	1.00	23.70
954	C	VAL	A	240	40.419	-15.640	-12.743	1.00	25.44
955	O	VAL	A	240	40.437	-15.350	-11.538	1.00	23.90
956	CB	VAL	A	240	38.369	-14.708	-13.849	1.00	22.65
957	CG1	VAL	A	240	39.170	-13.901	-14.866	1.00	22.07

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958	CG2	VAL	A	240	36.957	-14.947	-14.404	1.00	21.34
959	N	THR	A	241	41.505	-15.654	-13.524	1.00	24.76
960	CA	THR	A	241	42.835	-15.308	-13.067	1.00	26.11
961	C	THR	A	241	43.244	-13.957	-13.689	1.00	26.23
962	O	THR	A	241	43.165	-13.786	-14.922	1.00	24.94
963	CB	THR	A	241	43.856	-16.397	-13.451	1.00	26.92
964	OG1	THR	A	241	43.594	-17.610	-12.693	1.00	29.26
965	CG2	THR	A	241	45.285	-15.969	-13.169	1.00	25.11
966	N	PHE	A	242	43.659	-13.013	-12.870	1.00	23.69
967	CA	PHE	A	242	44.060	-11.655	-13.229	1.00	22.06
968	C	PHE	A	242	45.557	-11.465	-12.984	1.00	22.71
969	O	PHE	A	242	46.093	-11.901	-11.969	1.00	22.30
970	CB	PHE	A	242	43.275	-10.648	-12.369	1.00	22.34
971	CG	PHE	A	242	41.777	-10.695	-12.505	1.00	22.23
972	CD1	PHE	A	242	41.137	-9.866	-13.423	1.00	21.94
973	CD2	PHE	A	242	40.996	-11.545	-11.747	1.00	22.13
974	CE1	PHE	A	242	39.763	-9.870	-13.559	1.00	21.82
975	CE2	PHE	A	242	39.622	-11.580	-11.923	1.00	21.18
976	CZ	PHE	A	242	38.986	-10.744	-12.823	1.00	21.58
977	N	THR	A	243	46.285	-10.845	-13.922	1.00	20.68
978	CA	THR	A	243	47.718	-10.737	-13.888	1.00	21.11
979	C	THR	A	243	48.264	-9.334	-14.094	1.00	21.20
980	O	THR	A	243	47.787	-8.652	-14.989	1.00	19.64
981	CB	THR	A	243	48.327	-11.664	-14.974	1.00	22.96
982	OG1	THR	A	243	47.919	-13.047	-14.785	1.00	24.34
983	CG2	THR	A	243	49.846	-11.654	-14.938	1.00	23.70
984	N	TYR	A	244	49.357	-8.991	-13.418	1.00	21.69
985	CA	TYR	A	244	50.053	-7.712	-13.568	1.00	22.20
986	C	TYR	A	244	51.558	-7.971	-13.653	1.00	22.75
987	O	TYR	A	244	52.094	-8.753	-12.862	1.00	23.82
988	CB	TYR	A	244	49.763	-6.781	-12.377	1.00	22.63
989	CG	TYR	A	244	50.523	-5.466	-12.369	1.00	22.04
990	CD1	TYR	A	244	50.308	-4.453	-13.300	1.00	20.84
991	CD2	TYR	A	244	51.477	-5.248	-11.386	1.00	22.48
992	CE1	TYR	A	244	51.053	-3.287	-13.268	1.00	21.71
993	CE2	TYR	A	244	52.175	-4.046	-11.292	1.00	22.10
994	CZ	TYR	A	244	51.961	-3.071	-12.249	1.00	21.72
995	OH	TYR	A	244	52.682	-1.888	-12.195	1.00	21.67
996	N	ILE	A	245	52.258	-7.381	-14.614	1.00	21.91
997	CA	ILE	A	245	53.672	-7.500	-14.845	1.00	21.21
998	C	ILE	A	245	54.326	-6.151	-14.564	1.00	22.31
999	O	ILE	A	245	54.133	-5.163	-15.266	1.00	20.02
1000	CB	ILE	A	245	53.947	-7.953	-16.298	1.00	22.59
1001	CG1	ILE	A	245	53.225	-9.298	-16.560	1.00	23.96
1002	CG2	ILE	A	245	55.434	-8.035	-16.554	1.00	18.24
1003	CD1	ILE	A	245	53.736	-10.007	-17.795	1.00	27.43
1004	N	PRO	A	246	54.950	-6.024	-13.382	1.00	23.34
1005	CA	PRO	A	246	55.533	-4.759	-12.930	1.00	23.67
1006	C	PRO	A	246	56.506	-4.124	-13.911	1.00	22.46
1007	O	PRO	A	246	56.416	-2.914	-14.115	1.00	22.69
1008	CB	PRO	A	246	56.242	-5.151	-11.622	1.00	23.64
1009	CG	PRO	A	246	55.416	-6.302	-11.119	1.00	22.55
1010	CD	PRO	A	246	55.177	-7.102	-12.400	1.00	23.30
1011	N	SER	A	247	57.418	-4.864	-14.543	1.00	21.20
1012	CA	SER	A	247	58.360	-4.243	-15.475	1.00	23.73
1013	C	SER	A	247	57.762	-3.511	-16.663	1.00	24.65
1014	O	SER	A	247	58.401	-2.582	-17.178	1.00	24.40
1015	CB	SER	A	247	59.408	-5.238	-16.041	1.00	23.42
1016	OG	SER	A	247	58.758	-6.211	-16.858	1.00	23.25
1017	N	THR	A	248	56.656	-3.993	-17.221	1.00	23.91
1018	CA	THR	A	248	56.010	-3.307	-18.332	1.00	23.41
1019	C	THR	A	248	54.687	-2.652	-17.942	1.00	23.60
1020	O	THR	A	248	54.054	-1.971	-18.736	1.00	21.55
1021	CB	THR	A	248	55.680	-4.349	-19.443	1.00	22.17
1022	OG1	THR	A	248	54.807	-5.326	-18.855	1.00	17.24
1023	CG2	THR	A	248	56.993	-5.005	-19.903	1.00	21.11
1024	N	ASN	A	249	54.184	-2.889	-16.740	1.00	22.61
1025	CA	ASN	A	249	52.883	-2.425	-16.291	1.00	22.91
1026	C	ASN	A	249	51.737	-3.081	-17.080	1.00	20.56
1027	O	ASN	A	249	50.625	-2.569	-16.955	1.00	20.56
1028	CB	ASN	A	249	52.698	-0.900	-16.304	1.00	22.75
1029	CG	ASN	A	249	53.754	-0.182	-15.455	1.00	25.70
1030	OD1	ASN	A	249	53.878	-0.393	-14.245	1.00	24.53
1031	ND2	ASN	A	249	54.530	0.640	-16.173	1.00	24.05
1032	N	GLN	A	250	51.886	-4.178	-17.796	1.00	22.09
1033	CA	GLN	A	250	50.791	-4.759	-18.599	1.00	21.69
1034	C	GLN	A	250	49.829	-5.589	-17.734	1.00	22.85
1035	O	GLN	A	250	50.263	-6.152	-16.701	1.00	20.61
1036	CB	GLN	A	250	51.375	-5.611	-19.720	1.00	22.60
1037	CG	GLN	A	250	52.265	-4.859	-20.720	1.00	23.80
1038	CD	GLN	A	250	51.509	-3.725	-21.387	1.00	25.16
1039	OE1	GLN	A	250	50.566	-3.959	-22.167	1.00	24.30
1040	NE2	GLN	A	250	51.806	-2.490	-20.991	1.00	25.44
1041	N	VAL	A	251	48.526	-5.568	-18.077	1.00	21.86
1042	CA	VAL	A	251	47.558	-6.304	-17.262	1.00	21.68
1043	C	VAL	A	251	46.690	-7.203	-18.149	1.00	21.54
1044	O	VAL	A	251	46.351	-6.836	-19.273	1.00	19.04
1045	CB	VAL	A	251	46.680	-5.498	-16.291	1.00	23.56
1046	CG1	VAL	A	251	47.093	-4.039	-16.093	1.00	22.08
1047	CG2	VAL	A	251	45.175	-5.587	-16.451	1.00	22.66
1048	N	PHE	A	252	46.486	-8.436	-17.687	1.00	20.51
1049	CA	PHE	A	252	45.764	-9.449	-18.458	1.00	21.29
1050	C	PHE	A	252	44.747	-10.183	-17.592	1.00	22.46
1051	O	PHE	A	252	44.936	-10.267	-16.368	1.00	24.63
1052	CB	PHE	A	252	46.763	-10.520	-18.984	1.00	18.87
1053	CG	PHE	A	252	47.927	-9.918	-19.740	1.00	19.77

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1054	CD1	PHE	A	252	47.771	-9.602	-21.089	1.00	19.15
1055	CD2	PHE	A	252	49.087	-9.536	-19.076	1.00	19.82
1056	CE1	PHE	A	252	48.807	-9.007	-21.784	1.00	18.25
1057	CE2	PHE	A	252	50.125	-8.926	-19.777	1.00	21.04
1058	CZ	PHE	A	252	49.981	-8.666	-21.127	1.00	19.76
1059	N	ASP	A	253	43.766	-10.823	-18.207	1.00	21.21
1060	CA	ASP	A	253	42.883	-11.739	-17.490	1.00	21.71
1061	C	ASP	A	253	42.766	-13.015	-18.357	1.00	23.08
1062	O	ASP	A	253	42.922	-12.971	-19.582	1.00	20.43
1063	CB	ASP	A	253	41.525	-11.192	-17.091	1.00	22.08
1064	CG	ASP	A	253	40.668	-10.833	-18.296	1.00	23.51
1065	OD1	ASP	A	253	40.153	-11.833	-18.864	1.00	23.59
1066	OD2	ASP	A	253	40.550	-9.643	-18.650	1.00	22.42
1067	N	SER	A	254	42.493	-14.153	-17.717	1.00	21.89
1068	CA	SER	A	254	42.414	-15.435	-18.370	1.00	23.57
1069	C	SER	A	254	41.210	-15.586	-19.294	1.00	25.86
1070	O	SER	A	254	41.180	-16.566	-20.049	1.00	25.58
1071	CB	SER	A	254	42.435	-16.597	-17.360	1.00	23.34
1072	OG	SER	A	254	41.247	-16.555	-16.579	1.00	24.91
1073	N	VAL	A	255	40.213	-14.721	-19.243	1.00	26.09
1074	CA	VAL	A	255	39.076	-14.799	-20.148	1.00	28.53
1075	C	VAL	A	255	39.390	-14.071	-21.453	1.00	27.79
1076	O	VAL	A	255	39.341	-14.648	-22.555	1.00	26.52
1077	CB	VAL	A	255	37.816	-14.186	-19.501	1.00	30.76
1078	CG1	VAL	A	255	36.638	-14.033	-20.441	1.00	31.26
1079	CG2	VAL	A	255	37.385	-14.972	-18.275	1.00	31.36
1080	N	ASN	A	256	39.792	-12.806	-21.335	1.00	25.55
1081	CA	ASN	A	256	40.178	-12.043	-22.536	1.00	25.41
1082	C	ASN	A	256	41.509	-12.509	-23.144	1.00	27.70
1083	O	ASN	A	256	41.629	-12.355	-24.377	1.00	26.77
1084	CB	ASN	A	256	40.271	-10.550	-22.245	1.00	24.63
1085	CG	ASN	A	256	38.942	-9.900	-21.914	1.00	24.57
1086	OD1	ASN	A	256	38.017	-9.952	-22.712	1.00	24.02
1087	ND2	ASN	A	256	38.809	-9.279	-20.740	1.00	26.72
1088	N	HIS	A	257	42.432	-13.073	-22.365	1.00	25.02
1089	CA	HIS	A	257	43.727	-13.532	-22.914	1.00	26.70
1090	C	HIS	A	257	44.127	-14.879	-22.303	1.00	25.24
1091	O	HIS	A	257	44.864	-14.982	-21.322	1.00	22.57
1092	CB	HIS	A	257	44.801	-12.505	-22.514	1.00	27.64
1093	CG	HIS	A	257	46.027	-12.421	-23.350	1.00	31.69
1094	ND1	HIS	A	257	46.809	-13.517	-23.674	1.00	33.57
1095	CD2	HIS	A	257	46.623	-11.354	-23.934	1.00	31.77
1096	CE1	HIS	A	257	47.830	-13.122	-24.433	1.00	34.40
1097	NE2	HIS	A	257	47.743	-11.807	-24.598	1.00	34.33
1098	N	PRO	A	258	43.641	-15.986	-22.850	1.00	26.17
1099	CA	PRO	A	258	43.867	-17.303	-22.260	1.00	26.23
1100	C	PRO	A	258	45.227	-17.896	-22.590	1.00	26.44
1101	O	PRO	A	258	45.420	-18.723	-23.495	1.00	24.80
1102	CB	PRO	A	258	42.694	-18.124	-22.806	1.00	27.73
1103	CG	PRO	A	258	42.303	-17.456	-24.089	1.00	27.71
1104	CD	PRO	A	258	42.602	-15.992	-23.915	1.00	25.96
1105	N	ASN	A	259	46.254	-17.533	-21.821	1.00	26.95
1106	CA	ASN	A	259	47.623	-18.021	-21.925	1.00	25.18
1107	C	ASN	A	259	48.347	-17.710	-20.611	1.00	25.96
1108	O	ASN	A	259	48.451	-16.546	-20.208	1.00	26.02
1109	CB	ASN	A	259	48.371	-17.392	-23.103	1.00	25.42
1110	CG	ASN	A	259	49.814	-17.787	-23.316	1.00	25.25
1111	OD1	ASN	A	259	50.440	-17.469	-24.364	1.00	28.24
1112	ND2	ASN	A	259	50.464	-18.457	-22.388	1.00	23.35
1113	N	GLN	A	260	48.760	-18.771	-19.919	1.00	25.82
1114	CA	GLN	A	260	49.491	-18.660	-18.660	1.00	24.61
1115	C	GLN	A	260	50.983	-18.858	-18.828	1.00	25.53
1116	O	GLN	A	260	51.682	-18.938	-17.782	1.00	26.85
1117	CB	GLN	A	260	48.992	-19.714	-17.639	1.00	22.83
1118	CG	GLN	A	260	47.560	-19.480	-17.212	1.00	23.92
1119	CD	GLN	A	260	47.324	-18.192	-16.433	1.00	24.42
1120	OE1	GLN	A	260	47.977	-17.871	-15.455	1.00	22.77
1121	NE2	GLN	A	260	46.320	-17.451	-16.908	1.00	24.04
1122	N	ALA	A	261	51.524	-18.902	-20.070	1.00	24.54
1123	CA	ALA	A	261	52.993	-19.039	-20.165	1.00	24.10
1124	C	ALA	A	261	53.724	-17.709	-19.962	1.00	23.98
1125	O	ALA	A	261	54.494	-17.243	-20.832	1.00	22.89
1126	CB	ALA	A	261	53.400	-19.687	-21.497	1.00	22.32
1127	N	PHE	A	262	53.543	-17.054	-18.836	1.00	24.03
1128	CA	PHE	A	262	54.150	-15.787	-18.465	1.00	24.14
1129	C	PHE	A	262	55.652	-15.897	-18.208	1.00	25.13
1130	O	PHE	A	262	56.198	-16.920	-17.778	1.00	23.35
1131	CB	PHE	A	262	53.411	-15.253	-17.213	1.00	22.37
1132	CG	PHE	A	262	52.022	-14.753	-17.488	1.00	22.59
1133	CD1	PHE	A	262	50.911	-15.437	-17.022	1.00	22.84
1134	CD2	PHE	A	262	51.816	-13.575	-18.202	1.00	22.43
1135	CE1	PHE	A	262	49.624	-14.989	-17.269	1.00	21.45
1136	CE2	PHE	A	262	50.541	-13.133	-18.472	1.00	22.97
1137	CZ	PHE	A	262	49.440	-13.813	-18.003	1.00	22.36
1138	N	PRO	A	263	56.379	-14.800	-18.443	1.00	25.77
1139	CA	PRO	A	263	57.810	-14.746	-18.276	1.00	27.78
1140	C	PRO	A	263	58.230	-14.812	-16.809	1.00	29.38
1141	O	PRO	A	263	57.444	-14.598	-15.893	1.00	26.79
1142	CB	PRO	A	263	58.220	-13.454	-18.976	1.00	27.35
1143	CG	PRO	A	263	57.026	-12.629	-19.136	1.00	25.87
1144	CD	PRO	A	263	55.836	-13.514	-18.913	1.00	27.36
1145	N	THR	A	264	59.466	-15.244	-16.602	1.00	31.59
1146	CA	THR	A	264	60.041	-15.460	-15.284	1.00	34.76
1147	C	THR	A	264	61.224	-14.566	-14.986	1.00	35.79
1148	O	THR	A	264	61.745	-14.682	-13.867	1.00	37.84
1149	CB	THR	A	264	60.547	-16.920	-15.177	1.00	35.70

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1150	OG1	THR	A	264	61.354	-17.199	-16.330	1.00	37.91
1151	CG2	THR	A	264	59.441	-17.952	-15.205	1.00	36.80
1152	N	SER	A	265	61.739	-13.812	-15.944	1.00	35.41
1153	CA	SER	A	265	62.935	-13.002	-15.805	1.00	36.21
1154	C	SER	A	265	62.656	-11.549	-15.439	1.00	37.19
1155	O	SER	A	265	61.609	-10.978	-15.750	1.00	38.21
1156	CB	SER	A	265	63.740	-13.074	-17.100	1.00	36.57
1157	OG	SER	A	265	64.697	-12.050	-17.291	1.00	35.80
1158	N	SER	A	266	63.601	-10.915	-14.750	1.00	35.57
1159	CA	SER	A	266	63.488	-9.539	-14.271	1.00	34.73
1160	C	SER	A	266	64.355	-8.615	-15.113	1.00	35.65
1161	O	SER	A	266	64.631	-7.441	-14.841	1.00	33.89
1162	CB	SER	A	266	63.830	-9.438	-12.779	1.00	33.46
1163	OG	SER	A	266	62.821	-10.053	-11.983	1.00	33.15
1164	N	ALA	A	267	64.865	-9.185	-16.221	1.00	36.92
1165	CA	ALA	A	267	65.657	-8.374	-17.145	1.00	38.86
1166	C	ALA	A	267	64.766	-7.194	-17.577	1.00	40.22
1167	O	ALA	A	267	63.560	-7.315	-17.771	1.00	38.69
1168	CB	ALA	A	267	66.132	-9.162	-18.339	1.00	39.06
1169	N	GLY	A	268	65.403	-6.030	-17.573	1.00	42.28
1170	CA	GLY	A	268	64.752	-4.784	-17.865	1.00	44.37
1171	C	GLY	A	268	64.348	-3.978	-16.643	1.00	46.77
1172	O	GLY	A	268	64.299	-2.737	-16.795	1.00	47.62
1173	N	VAL	A	269	64.052	-4.595	-15.480	1.00	46.24
1174	CA	VAL	A	269	63.594	-3.736	-14.385	1.00	45.82
1175	C	VAL	A	269	64.666	-2.835	-13.801	1.00	44.79
1176	O	VAL	A	269	65.871	-3.071	-13.802	1.00	44.61
1177	CB	VAL	A	269	62.762	-4.389	-13.300	1.00	47.26
1178	CG1	VAL	A	269	61.276	-4.187	-13.663	1.00	47.77
1179	CG2	VAL	A	269	62.947	-5.864	-13.074	1.00	47.82
1180	N	GLN	A	270	64.168	-1.666	-13.364	1.00	44.38
1181	CA	GLN	A	270	65.117	-0.651	-12.866	1.00	43.41
1182	C	GLN	A	270	65.016	-0.541	-11.348	1.00	39.99
1183	O	GLN	A	270	63.909	-0.536	-10.823	1.00	39.03
1184	CB	GLN	A	270	64.909	0.628	-13.663	1.00	44.70
1185	CG	GLN	A	270	63.545	1.259	-13.564	1.00	46.40
1186	CD	GLN	A	270	63.594	2.718	-14.049	1.00	48.21
1187	OE1	GLN	A	270	63.352	3.648	-13.263	1.00	49.65
1188	NE2	GLN	A	270	63.949	2.916	-15.320	1.00	47.11
1189	N	THR	A	271	66.168	-0.620	-10.661	1.00	36.93
1190	CA	THR	A	271	66.136	-0.641	-9.198	1.00	32.17
1191	C	THR	A	271	67.457	-0.271	-8.565	1.00	31.16
1192	O	THR	A	271	68.558	-0.403	-9.078	1.00	29.69
1193	CB	THR	A	271	65.681	-2.033	-8.683	1.00	32.24
1194	OG1	THR	A	271	65.608	-2.075	-7.243	1.00	30.97
1195	CG2	THR	A	271	66.584	-3.179	-9.133	1.00	30.31
1196	N	ASN	A	272	67.330	0.245	-7.332	1.00	28.98
1197	CA	ASN	A	272	68.481	0.558	-6.529	1.00	26.71
1198	C	ASN	A	272	68.527	-0.399	-5.322	1.00	24.87
1199	O	ASN	A	272	69.417	-0.272	-4.515	1.00	22.11
1200	CB	ASN	A	272	68.464	2.031	-6.162	1.00	27.42
1201	CG	ASN	A	272	67.423	2.457	-5.152	1.00	27.32
1202	OD1	ASN	A	272	67.473	3.640	-4.735	1.00	28.32
1203	ND2	ASN	A	272	66.516	1.631	-4.751	1.00	25.56
1204	N	LEU	A	273	67.770	-1.488	-5.320	1.00	24.32
1205	CA	LEU	A	273	67.740	-2.431	-4.206	1.00	24.89
1206	C	LEU	A	273	67.477	-3.819	-4.758	1.00	24.94
1207	O	LEU	A	273	66.401	-4.035	-5.326	1.00	23.57
1208	CB	LEU	A	273	66.640	-2.010	-3.197	1.00	25.97
1209	CG	LEU	A	273	66.566	-2.816	-1.893	1.00	24.77
1210	CD1	LEU	A	273	67.763	-2.539	-0.981	1.00	23.86
1211	CD2	LEU	A	273	65.279	-2.514	-1.136	1.00	25.15
1212	N	VAL	A	274	68.455	-4.706	-4.675	1.00	24.94
1213	CA	VAL	A	274	68.417	-5.999	-5.341	1.00	26.05
1214	C	VAL	A	274	68.515	-7.184	-4.379	1.00	26.04
1215	O	VAL	A	274	69.229	-7.097	-3.381	1.00	26.70
1216	CB	VAL	A	274	69.583	-6.171	-6.361	1.00	25.86
1217	CG1	VAL	A	274	69.620	-5.082	-7.432	1.00	25.76
1218	CG2	VAL	A	274	70.921	-6.116	-5.640	1.00	26.10
1219	N	GLN	A	275	67.836	-8.261	-4.692	1.00	25.69
1220	CA	GLN	A	275	67.948	-9.534	-4.016	1.00	27.38
1221	C	GLN	A	275	68.722	-10.509	-4.924	1.00	26.18
1222	O	GLN	A	275	68.335	-10.671	-6.064	1.00	24.99
1223	CB	GLN	A	275	66.596	-10.143	-3.662	1.00	26.97
1224	CG	GLN	A	275	66.671	-11.477	-2.930	1.00	28.59
1225	CD	GLN	A	275	65.265	-11.964	-2.607	1.00	32.32
1226	OE1	GLN	A	275	64.501	-11.303	-1.895	1.00	33.16
1227	NE2	GLN	A	275	64.893	-13.118	-3.136	1.00	32.96
1228	N	LEU	A	276	69.837	-11.012	-4.427	1.00	25.42
1229	CA	LEU	A	276	70.697	-11.944	-5.130	1.00	25.50
1230	C	LEU	A	276	70.562	-13.358	-4.573	1.00	26.02
1231	O	LEU	A	276	70.448	-13.492	-3.342	1.00	26.72
1232	CB	LEU	A	276	72.157	-11.498	-5.051	1.00	23.09
1233	CG	LEU	A	276	72.473	-10.046	-5.406	1.00	24.38
1234	CD1	LEU	A	276	73.930	-9.640	-5.129	1.00	23.10
1235	CD2	LEU	A	276	72.173	-9.799	-6.886	1.00	22.76
1236	N	THR	A	277	70.615	-14.370	-5.434	1.00	25.00
1237	CA	THR	A	277	70.574	-15.758	-5.009	1.00	24.89
1238	C	THR	A	277	71.967	-16.301	-5.329	1.00	25.72
1239	O	THR	A	277	72.476	-15.942	-6.401	1.00	26.30
1240	CB	THR	A	277	69.479	-16.586	-5.694	1.00	27.01
1241	OG1	THR	A	277	68.199	-15.975	-5.436	1.00	27.31
1242	CG2	THR	A	277	69.423	-18.028	-5.179	1.00	25.75
1243	N	LEU	A	278	72.567	-17.086	-4.445	1.00	24.33
1244	CA	LEU	A	278	73.924	-17.581	-4.635	1.00	24.69
1245	C	LEU	A	278	73.883	-19.074	-4.953	1.00	25.40

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1246	O	LEU	A	278	72.925	-19.707	-4.513	1.00	25.92
1247	CB	LEU	A	278	74.755	-17.375	-3.349	1.00	24.44
1248	CG	LEU	A	278	74.785	-15.959	-2.779	1.00	25.93
1249	CD1	LEU	A	278	75.676	-15.830	-1.528	1.00	25.09
1250	CD2	LEU	A	278	75.228	-14.960	-3.842	1.00	25.13
1251	N	ALA	A	279	74.866	-19.602	-5.666	1.00	25.25
1252	CA	ALA	A	279	74.847	-21.038	-5.956	1.00	27.68
1253	C	ALA	A	279	75.156	-21.861	-4.701	1.00	26.75
1254	O	ALA	A	279	74.770	-23.030	-4.671	1.00	25.73
1255	CB	ALA	A	279	75.804	-21.373	-7.095	1.00	27.60
1256	N	SER	A	280	75.918	-21.347	-3.736	1.00	26.02
1257	CA	SER	A	280	76.117	-22.146	-2.509	1.00	28.04
1258	C	SER	A	280	76.067	-21.219	-1.293	1.00	27.40
1259	O	SER	A	280	76.144	-19.994	-1.449	1.00	27.94
1260	CB	SER	A	280	77.417	-22.948	-2.579	1.00	27.93
1261	OG	SER	A	280	78.501	-22.049	-2.693	1.00	27.71
1262	N	ALA	A	281	75.919	-21.724	-0.101	1.00	26.67
1263	CA	ALA	A	281	75.824	-20.907	1.108	1.00	26.36
1264	C	ALA	A	281	77.169	-20.545	1.709	1.00	26.18
1265	O	ALA	A	281	77.935	-21.377	2.183	1.00	25.41
1266	CB	ALA	A	281	75.004	-21.695	2.132	1.00	26.66
1267	N	PRO	A	282	77.452	-19.248	1.797	1.00	27.13
1268	CA	PRO	A	282	78.677	-18.742	2.392	1.00	27.03
1269	C	PRO	A	282	78.792	-19.115	3.866	1.00	26.41
1270	O	PRO	A	282	77.776	-19.312	4.518	1.00	24.07
1271	CB	PRO	A	282	78.587	-17.226	2.229	1.00	26.75
1272	CG	PRO	A	282	77.126	-16.962	2.093	1.00	28.81
1273	CD	PRO	A	282	76.589	-18.131	1.316	1.00	27.00
1274	N	ASP	A	283	80.031	-19.217	4.332	1.00	24.52
1275	CA	ASP	A	283	80.333	-19.422	5.754	1.00	24.81
1276	C	ASP	A	283	80.147	-18.073	6.436	1.00	22.38
1277	O	ASP	A	283	80.864	-17.107	6.145	1.00	21.69
1278	CB	ASP	A	283	81.775	-19.935	5.887	1.00	25.32
1279	CG	ASP	A	283	82.210	-20.254	7.297	1.00	25.30
1280	OD1	ASP	A	283	82.960	-21.237	7.484	1.00	25.14
1281	OD2	ASP	A	283	81.801	-19.536	8.239	1.00	25.29
1282	N	VAL	A	284	79.206	-17.940	7.380	1.00	22.67
1283	CA	VAL	A	284	78.952	-16.654	8.035	1.00	22.22
1284	C	VAL	A	284	80.074	-16.100	8.887	1.00	24.45
1285	O	VAL	A	284	80.021	-14.907	9.268	1.00	24.83
1286	CB	VAL	A	284	77.642	-16.672	8.867	1.00	22.56
1287	CG1	VAL	A	284	76.463	-17.083	7.976	1.00	19.20
1288	CG2	VAL	A	284	77.712	-17.517	10.125	1.00	19.74
1289	N	THR	A	285	81.154	-16.864	9.118	1.00	22.48
1290	CA	THR	A	285	82.292	-16.304	9.840	1.00	22.60
1291	C	THR	A	285	83.379	-15.770	8.912	1.00	22.76
1292	O	THR	A	285	84.414	-15.336	9.433	1.00	23.50
1293	CB	THR	A	285	82.906	-17.394	10.742	1.00	22.23
1294	OG1	THR	A	285	83.613	-18.376	9.942	1.00	22.05
1295	CG2	THR	A	285	81.829	-18.132	11.529	1.00	19.25
1296	N	HIS	A	286	83.257	-15.892	7.608	1.00	23.16
1297	CA	HIS	A	286	84.273	-15.462	6.656	1.00	24.10
1298	C	HIS	A	286	84.119	-14.015	6.202	1.00	23.79
1299	O	HIS	A	286	83.119	-13.382	6.557	1.00	20.85
1300	CB	HIS	A	286	84.336	-16.407	5.450	1.00	25.64
1301	CG	HIS	A	286	85.025	-17.700	5.781	1.00	26.97
1302	ND1	HIS	A	286	85.197	-18.702	4.857	1.00	27.65
1303	CD2	HIS	A	286	85.496	-18.195	6.960	1.00	27.96
1304	CE1	HIS	A	286	85.827	-19.731	5.390	1.00	27.73
1305	NE2	HIS	A	286	86.003	-19.451	6.664	1.00	29.50
1306	N	ASN	A	287	85.074	-13.467	5.472	1.00	23.23
1307	CA	ASN	A	287	85.032	-12.068	5.021	1.00	26.78
1308	C	ASN	A	287	84.421	-12.025	3.625	1.00	26.70
1309	O	ASN	A	287	85.103	-12.453	2.685	1.00	26.28
1310	CB	ASN	A	287	86.459	-11.491	4.965	1.00	29.01
1311	CG	ASN	A	287	86.508	-10.068	4.447	1.00	30.90
1312	OD1	ASN	A	287	85.558	-9.293	4.551	1.00	31.63
1313	ND2	ASN	A	287	87.625	-9.643	3.861	1.00	32.44
1314	N	LEU	A	288	83.160	-11.657	3.461	1.00	25.67
1315	CA	LEU	A	288	82.489	-11.815	2.175	1.00	25.40
1316	C	LEU	A	288	82.186	-10.519	1.449	1.00	26.53
1317	O	LEU	A	288	81.557	-9.651	2.046	1.00	26.44
1318	CB	LEU	A	288	81.178	-12.587	2.402	1.00	24.27
1319	CG	LEU	A	288	81.251	-13.809	3.317	1.00	24.57
1320	CD1	LEU	A	288	79.857	-14.127	3.887	1.00	26.43
1321	CD2	LEU	A	288	81.787	-15.040	2.602	1.00	24.91
1322	N	ASP	A	289	82.547	-10.452	0.170	1.00	26.00
1323	CA	ASP	A	289	82.295	-9.192	-0.541	1.00	28.88
1324	C	ASP	A	289	81.371	-9.408	-1.731	1.00	26.48
1325	O	ASP	A	289	81.368	-10.484	-2.310	1.00	26.03
1326	CB	ASP	A	289	83.633	-8.584	-0.985	1.00	33.27
1327	CG	ASP	A	289	84.133	-7.466	-0.104	1.00	36.80
1328	OD1	ASP	A	289	83.765	-7.242	1.063	1.00	38.78
1329	OD2	ASP	A	289	84.979	-6.701	-0.626	1.00	40.62
1330	N	VAL	A	290	80.617	-8.385	-2.091	1.00	25.24
1331	CA	VAL	A	290	79.774	-8.372	-3.271	1.00	25.70
1332	C	VAL	A	290	80.162	-7.119	-4.085	1.00	27.14
1333	O	VAL	A	290	80.498	-6.084	-3.527	1.00	26.07
1334	CB	VAL	A	290	78.259	-8.332	-2.999	1.00	24.55
1335	CG1	VAL	A	290	77.827	-7.147	-2.128	1.00	22.41
1336	CG2	VAL	A	290	77.423	-8.332	-4.289	1.00	23.49
1337	N	ALA	A	291	80.104	-7.252	-5.408	1.00	29.18
1338	CA	ALA	A	291	80.361	-6.141	-6.312	1.00	30.04
1339	C	ALA	A	291	79.519	-6.327	-7.579	1.00	30.92
1340	O	ALA	A	291	78.916	-7.386	-7.813	1.00	29.72
1341	CB	ALA	A	291	81.857	-6.093	-6.675	1.00	29.98

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1342	N	ALA	A	292	79.485	-5.297	-8.406	1.00 33.04
1343	CA	ALA	A	292	78.809	-5.359	-9.703	1.00 34.88
1344	C	ALA	A	292	79.590	-4.565	-10.738	1.00 36.66
1345	O	ALA	A	292	80.342	-3.645	-10.375	1.00 36.13
1346	CB	ALA	A	292	77.395	-4.832	-9.570	1.00 35.02
1347	N	ASP	A	293	79.430	-4.891	-12.019	1.00 39.96
1348	CA	ASP	A	293	80.165	-4.141	-13.054	1.00 42.63
1349	C	ASP	A	293	79.890	-2.644	-12.977	1.00 41.11
1350	O	ASP	A	293	78.750	-2.184	-13.100	1.00 41.97
1351	CB	ASP	A	293	79.817	-4.670	-14.451	1.00 46.42
1352	CG	ASP	A	293	80.532	-3.867	-15.535	1.00 49.75
1353	OD1	ASP	A	293	81.775	-3.978	-15.683	1.00 50.50
1354	OD2	ASP	A	293	79.821	-3.106	-16.246	1.00 51.35
1355	N	GLY	A	294	80.904	-1.835	-12.717	1.00 40.88
1356	CA	GLY	A	294	80.737	-0.390	-12.588	1.00 41.91
1357	C	GLY	A	294	80.525	0.114	-11.170	1.00 41.98
1358	O	GLY	A	294	80.616	1.353	-10.921	1.00 42.78
1359	N	TYR	A	295	80.314	-0.798	-10.204	1.00 39.89
1360	CA	TYR	A	295	80.112	-0.393	-8.813	1.00 38.42
1361	C	TYR	A	295	81.240	-0.871	-7.900	1.00 37.45
1362	O	TYR	A	295	81.573	-2.057	-7.972	1.00 38.33
1363	CB	TYR	A	295	78.808	-0.951	-8.238	1.00 36.42
1364	CG	TYR	A	295	77.510	-0.422	-8.776	1.00 35.08
1365	CD1	TYR	A	295	76.787	0.576	-8.131	1.00 33.65
1366	CD2	TYR	A	295	77.014	-0.921	-9.988	1.00 34.53
1367	CE1	TYR	A	295	75.587	1.055	-8.644	1.00 32.54
1368	CE2	TYR	A	295	75.851	-0.409	-10.548	1.00 33.98
1369	CZ	TYR	A	295	75.142	0.565	-9.856	1.00 33.30
1370	OH	TYR	A	295	73.963	1.007	-10.411	1.00 31.85
1371	N	LYS	A	296	81.795	-0.014	-7.051	1.00 36.68
1372	CA	LYS	A	296	82.757	-0.537	-6.079	1.00 36.58
1373	C	LYS	A	296	82.057	-1.439	-5.060	1.00 34.22
1374	O	LYS	A	296	80.894	-1.258	-4.694	1.00 31.79
1375	CB	LYS	A	296	83.624	0.497	-5.430	1.00 39.77
1376	CG	LYS	A	296	83.045	1.710	-4.813	1.00 43.12
1377	CD	LYS	A	296	82.983	1.676	-3.283	1.00 45.75
1378	CE	LYS	A	296	84.388	1.604	-2.699	1.00 47.63
1379	NZ	LYS	A	296	84.818	0.148	-2.669	1.00 48.54
1380	N	ALA	A	297	82.840	-2.431	-4.652	1.00 30.70
1381	CA	ALA	A	297	82.424	-3.491	-3.761	1.00 28.61
1382	C	ALA	A	297	82.078	-3.124	-2.319	1.00 28.36
1383	O	ALA	A	297	82.475	-2.094	-1.762	1.00 24.23
1384	CB	ALA	A	297	83.576	-4.498	-3.796	1.00 28.17
1385	N	HIS	A	298	81.359	-4.049	-1.654	1.00 25.58
1386	CA	HIS	A	298	81.044	-3.900	-0.241	1.00 25.55
1387	C	HIS	A	298	81.031	-5.260	0.470	1.00 22.74
1388	O	HIS	A	298	80.656	-6.242	-0.135	1.00 23.46
1389	CB	HIS	A	298	79.678	-3.242	-0.038	1.00 25.93
1390	CG	HIS	A	298	79.409	-2.728	1.343	1.00 24.84
1391	ND1	HIS	A	298	79.527	-1.366	1.547	1.00 25.94
1392	CD2	HIS	A	298	79.039	-3.239	2.536	1.00 22.97
1393	CE1	HIS	A	298	79.249	-1.045	2.793	1.00 24.28
1394	NE2	HIS	A	298	78.944	-2.172	3.412	1.00 23.71
1395	N	ASN	A	299	81.383	-5.265	1.739	1.00 22.36
1396	CA	ASN	A	299	81.334	-6.364	2.665	1.00 22.13
1397	C	ASN	A	299	79.897	-6.847	2.839	1.00 20.98
1398	O	ASN	A	299	78.992	-6.014	2.842	1.00 17.58
1399	CB	ASN	A	299	81.878	-5.915	4.056	1.00 22.29
1400	CG	ASN	A	299	81.745	-7.085	5.033	1.00 22.68
1401	OD1	ASN	A	299	82.457	-8.091	4.922	1.00 23.89
1402	ND2	ASN	A	299	80.826	-6.978	5.967	1.00 22.28
1403	N	ILE	A	300	79.663	-8.134	2.970	1.00 19.88
1404	CA	ILE	A	300	78.342	-8.681	3.200	1.00 21.29
1405	C	ILE	A	300	78.204	-9.065	4.694	1.00 20.22
1406	O	ILE	A	300	78.956	-9.925	5.183	1.00 20.11
1407	CB	ILE	A	300	78.053	-9.924	2.344	1.00 20.62
1408	CG1	ILE	A	300	78.330	-9.621	0.866	1.00 21.23
1409	CG2	ILE	A	300	76.614	-10.380	2.533	1.00 21.02
1410	CD1	ILE	A	300	78.258	-10.831	-0.021	1.00 20.37
1411	N	LEU	A	301	77.336	-8.388	5.423	1.00 17.75
1412	CA	LEU	A	301	77.209	-8.699	6.870	1.00 18.06
1413	C	LEU	A	301	76.024	-9.630	7.119	1.00 17.18
1414	O	LEU	A	301	74.921	-9.397	6.603	1.00 15.63
1415	CB	LEU	A	301	77.007	-7.399	7.657	1.00 17.96
1416	CG	LEU	A	301	77.055	-7.516	9.198	1.00 19.15
1417	CD1	LEU	A	301	78.494	-7.470	9.695	1.00 17.41
1418	CD2	LEU	A	301	76.236	-6.376	9.814	1.00 17.81
1419	N	PRO	A	302	76.217	-10.719	7.848	1.00 15.47
1420	CA	PRO	A	302	75.088	-11.614	8.092	1.00 15.32
1421	C	PRO	A	302	74.052	-10.972	9.021	1.00 15.88
1422	O	PRO	A	302	74.372	-10.349	10.023	1.00 16.78
1423	CB	PRO	A	302	75.628	-12.891	8.738	1.00 14.74
1424	CG	PRO	A	302	77.150	-12.804	8.778	1.00 16.15
1425	CD	PRO	A	302	77.395	-11.247	8.517	1.00 15.56
1426	N	ARG	A	303	72.765	-11.115	8.636	1.00 14.90
1427	CA	ARG	A	303	71.700	-10.524	9.441	1.00 14.86
1428	C	ARG	A	303	70.536	-11.502	9.653	1.00 12.98
1429	O	ARG	A	303	70.394	-12.126	10.696	1.00 12.86
1430	CB	ARG	A	303	71.204	-9.270	8.718	1.00 15.19
1431	CG	ARG	A	303	69.950	-8.675	9.361	1.00 15.51
1432	CD	ARG	A	303	69.519	-7.377	8.675	1.00 16.61
1433	NE	ARG	A	303	68.772	-7.664	7.445	1.00 17.37
1434	CZ	ARG	A	303	67.916	-6.721	7.011	1.00 19.59
1435	NH1	ARG	A	303	67.775	-5.593	7.686	1.00 18.10
1436	NH2	ARG	A	303	67.226	-6.920	5.887	1.00 17.39
1437	N	ASN	A	304	69.665	-11.600	8.626	1.00 14.70

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1438	CA	ASN	A	304	68.496	-12.476	8.741	1.00	14.47
1439	C	ASN	A	304	68.829	-13.961	8.551	1.00	15.73
1440	O	ASN	A	304	68.090	-14.850	8.955	1.00	16.46
1441	CB	ASN	A	304	67.423	-12.026	7.748	1.00	14.98
1442	CG	ASN	A	304	66.623	-10.906	8.362	1.00	15.04
1443	OD1	ASN	A	304	66.852	-10.495	9.494	1.00	16.92
1444	ND2	ASN	A	304	65.660	-10.396	7.575	1.00	14.95
1445	N	VAL	A	305	69.997	-14.272	8.008	1.00	15.65
1446	CA	VAL	A	305	70.457	-15.659	7.877	1.00	15.60
1447	C	VAL	A	305	70.641	-16.261	9.281	1.00	14.99
1448	O	VAL	A	305	70.346	-17.453	9.542	1.00	13.78
1449	CB	VAL	A	305	71.763	-15.754	7.057	1.00	16.12
1450	CG1	VAL	A	305	72.886	-15.007	7.820	1.00	16.01
1451	CG2	VAL	A	305	72.211	-17.204	6.923	1.00	14.70
1452	N	LEU	A	306	70.943	-15.455	10.302	1.00	15.35
1453	CA	LEU	A	306	71.061	-15.925	11.682	1.00	16.85
1454	C	LEU	A	306	69.742	-16.291	12.359	1.00	16.79
1455	O	LEU	A	306	69.821	-16.866	13.444	1.00	16.11
1456	CB	LEU	A	306	71.854	-14.947	12.574	1.00	17.30
1457	CG	LEU	A	306	73.183	-14.497	11.943	1.00	18.98
1458	CD1	LEU	A	306	73.755	-13.292	12.719	1.00	21.71
1459	CD2	LEU	A	306	74.171	-15.623	11.853	1.00	17.50
1460	N	ASN	A	307	68.579	-16.074	11.742	1.00	17.17
1461	CA	ASN	A	307	67.295	-16.537	12.219	1.00	19.40
1462	C	ASN	A	307	67.118	-18.065	11.996	1.00	22.23
1463	O	ASN	A	307	66.235	-18.629	12.645	1.00	19.61
1464	CB	ASN	A	307	66.072	-15.914	11.520	1.00	17.50
1465	CG	ASN	A	307	65.952	-14.411	11.499	1.00	19.19
1466	OD1	ASN	A	307	66.604	-13.703	12.268	1.00	16.40
1467	ND2	ASN	A	307	65.093	-13.861	10.615	1.00	16.76
1468	N	LEU	A	308	67.846	-18.698	11.079	1.00	20.99
1469	CA	LEU	A	308	67.709	-20.121	10.793	1.00	20.83
1470	C	LEU	A	308	67.998	-21.006	11.995	1.00	21.03
1471	O	LEU	A	308	68.784	-20.723	12.906	1.00	18.48
1472	CB	LEU	A	308	68.641	-20.561	9.636	1.00	21.47
1473	CG	LEU	A	308	68.405	-19.861	8.291	1.00	23.03
1474	CD1	LEU	A	308	69.489	-20.134	7.261	1.00	23.09
1475	CD2	LEU	A	308	67.039	-20.248	7.739	1.00	21.71
1476	N	PRO	A	309	67.320	-22.166	12.049	1.00	20.22
1477	CA	PRO	A	309	67.416	-23.095	13.161	1.00	19.80
1478	C	PRO	A	309	68.812	-23.561	13.507	1.00	19.00
1479	O	PRO	A	309	69.113	-23.663	14.715	1.00	19.17
1480	CB	PRO	A	309	66.476	-24.256	12.793	1.00	20.37
1481	CG	PRO	A	309	65.446	-23.573	11.949	1.00	19.19
1482	CD	PRO	A	309	66.282	-22.609	11.100	1.00	19.26
1483	N	ARG	A	310	69.744	-23.653	12.564	1.00	18.57
1484	CA	ARG	A	310	71.114	-24.027	12.882	1.00	18.99
1485	C	ARG	A	310	71.813	-23.033	13.806	1.00	20.10
1486	O	ARG	A	310	72.758	-23.400	14.544	1.00	19.39
1487	CB	ARG	A	310	71.910	-24.244	11.582	1.00	21.29
1488	CG	ARG	A	310	72.315	-22.947	10.876	1.00	23.49
1489	CD	ARG	A	310	73.173	-23.235	9.648	1.00	25.45
1490	NE	ARG	A	310	74.564	-23.436	10.024	1.00	30.55
1491	CZ	ARG	A	310	75.583	-23.674	9.187	1.00	33.31
1492	NH1	ARG	A	310	75.463	-23.744	7.854	1.00	33.05
1493	NH2	ARG	A	310	76.793	-23.814	9.703	1.00	33.33
1494	N	TYR	A	311	71.378	-21.761	13.838	1.00	18.74
1495	CA	TYR	A	311	71.933	-20.818	14.800	1.00	19.14
1496	C	TYR	A	311	71.067	-20.575	16.024	1.00	19.76
1497	O	TYR	A	311	71.260	-19.550	16.682	1.00	19.20
1498	CB	TYR	A	311	72.119	-19.454	14.074	1.00	20.52
1499	CG	TYR	A	311	72.939	-19.630	12.795	1.00	20.06
1500	CD1	TYR	A	311	72.341	-19.445	11.558	1.00	19.78
1501	CD2	TYR	A	311	74.254	-20.025	12.854	1.00	19.22
1502	CE1	TYR	A	311	73.093	-19.612	10.395	1.00	21.56
1503	CE2	TYR	A	311	75.018	-20.203	11.703	1.00	20.95
1504	CZ	TYR	A	311	74.425	-19.993	10.480	1.00	21.56
1505	OH	TYR	A	311	75.159	-20.170	9.329	1.00	24.43
1506	N	ASP	A	312	70.069	-21.385	16.314	1.00	22.16
1507	CA	ASP	A	312	69.147	-21.132	17.421	1.00	24.33
1508	C	ASP	A	312	69.426	-21.956	18.667	1.00	22.29
1509	O	ASP	A	312	69.166	-23.155	18.676	1.00	22.82
1510	CB	ASP	A	312	67.703	-21.360	16.940	1.00	25.85
1511	CG	ASP	A	312	66.717	-20.989	18.046	1.00	30.43
1512	OD1	ASP	A	312	66.756	-19.889	18.609	1.00	30.37
1513	OD2	ASP	A	312	65.841	-21.814	18.382	1.00	33.45
1514	N	TYR	A	313	69.905	-21.325	19.725	1.00	21.56
1515	CA	TYR	A	313	70.305	-22.052	20.933	1.00	21.31
1516	C	TYR	A	313	69.224	-21.924	21.996	1.00	22.83
1517	O	TYR	A	313	68.987	-20.799	22.457	1.00	20.91
1518	CB	TYR	A	313	71.644	-21.503	21.452	1.00	20.67
1519	CG	TYR	A	313	72.137	-22.255	22.674	1.00	19.10
1520	CD1	TYR	A	313	72.697	-23.521	22.532	1.00	18.67
1521	CD2	TYR	A	313	71.998	-21.744	23.956	1.00	18.42
1522	CE1	TYR	A	313	73.148	-24.247	23.621	1.00	19.13
1523	CE2	TYR	A	313	72.416	-22.475	25.069	1.00	17.61
1524	CZ	TYR	A	313	72.994	-23.703	24.889	1.00	19.22
1525	OH	TYR	A	313	73.413	-24.442	25.989	1.00	18.27
1526	N	SER	A	314	68.599	-23.055	22.329	1.00	23.06
1527	CA	SER	A	314	67.542	-23.000	23.332	1.00	25.19
1528	C	SER	A	314	67.926	-23.474	24.719	1.00	25.25
1529	O	SER	A	314	67.000	-23.528	25.550	1.00	25.31
1530	CB	SER	A	314	66.307	-23.804	22.843	1.00	27.03
1531	OG	SER	A	314	66.672	-25.175	22.739	1.00	28.18
1532	N	GLY	A	315	69.182	-23.694	25.070	1.00	24.12
1533	CA	GLY	A	315	69.527	-24.093	26.451	1.00	24.72

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1534	C	GLY	A	315	69.338	-22.967	27.453	1.00	25.47
1535	O	GLY	A	315	69.165	-21.816	27.048	1.00	26.04
1536	N	ASN	A	316	69.339	-23.228	28.754	1.00	25.24
1537	CA	ASN	A	316	69.116	-22.249	29.805	1.00	25.73
1538	C	ASN	A	316	70.397	-21.804	30.509	1.00	25.95
1539	O	ASN	A	316	70.298	-21.278	31.638	1.00	24.29
1540	CB	ASN	A	316	68.190	-22.893	30.866	1.00	29.42
1541	CG	ASN	A	316	68.861	-23.980	31.705	1.00	33.78
1542	OD1	ASN	A	316	70.048	-24.341	31.528	1.00	33.72
1543	ND2	ASN	A	316	68.154	-24.553	32.687	1.00	34.41
1544	N	ASP	A	317	71.584	-22.038	29.911	1.00	21.74
1545	CA	ASP	A	317	72.807	-21.719	30.606	1.00	21.65
1546	C	ASP	A	317	73.650	-20.592	30.037	1.00	22.99
1547	O	ASP	A	317	74.868	-20.599	30.297	1.00	22.74
1548	CB	ASP	A	317	73.665	-23.009	30.705	1.00	22.71
1549	CG	ASP	A	317	74.073	-23.483	29.316	1.00	23.13
1550	OD1	ASP	A	317	73.271	-23.346	28.363	1.00	22.02
1551	OD2	ASP	A	317	75.185	-24.003	29.157	1.00	22.43
1552	N	LEU	A	318	73.097	-19.656	29.260	1.00	22.59
1553	CA	LEU	A	318	73.889	-18.531	28.754	1.00	20.66
1554	C	LEU	A	318	74.316	-17.676	29.955	1.00	20.42
1555	O	LEU	A	318	73.547	-17.564	30.903	1.00	17.61
1556	CB	LEU	A	318	73.169	-17.678	27.715	1.00	20.60
1557	CG	LEU	A	318	72.798	-18.391	26.385	1.00	19.68
1558	CD1	LEU	A	318	71.963	-17.493	25.495	1.00	17.29
1559	CD2	LEU	A	318	74.109	-18.776	25.680	1.00	16.96
1560	N	GLY	A	319	75.550	-17.187	29.890	1.00	20.73
1561	CA	GLY	A	319	76.193	-16.428	30.949	1.00	20.43
1562	C	GLY	A	319	77.202	-17.295	31.721	1.00	22.10
1563	O	GLY	A	319	77.914	-18.124	31.117	1.00	21.40
1564	N	ASN	A	320	77.286	-17.098	33.042	1.00	19.98
1565	CA	ASN	A	320	78.191	-17.952	33.835	1.00	21.91
1566	C	ASN	A	320	77.375	-18.729	34.867	1.00	22.53
1567	O	ASN	A	320	76.333	-18.231	35.331	1.00	21.27
1568	CB	ASN	A	320	79.297	-17.159	34.508	1.00	21.04
1569	CG	ASN	A	320	78.807	-16.191	35.571	1.00	21.43
1570	OD1	ASN	A	320	78.574	-16.655	36.680	1.00	22.62
1571	ND2	ASN	A	320	78.589	-14.900	35.304	1.00	18.58
1572	N	VAL	A	321	77.797	-19.940	35.176	1.00	22.76
1573	CA	VAL	A	321	77.084	-20.812	36.124	1.00	22.43
1574	C	VAL	A	321	78.113	-21.225	37.192	1.00	24.11
1575	O	VAL	A	321	78.998	-22.018	36.899	1.00	23.74
1576	CB	VAL	A	321	76.477	-22.041	35.464	1.00	24.06
1577	CG1	VAL	A	321	75.861	-23.044	36.476	1.00	25.33
1578	CG2	VAL	A	321	75.396	-21.628	34.452	1.00	23.25
1579	N	TYR	A	322	78.040	-20.600	38.364	1.00	24.47
1580	CA	TYR	A	322	79.021	-20.745	39.416	1.00	26.10
1581	C	TYR	A	322	78.764	-21.897	40.382	1.00	26.90
1582	O	TYR	A	322	77.658	-22.184	40.816	1.00	25.89
1583	CB	TYR	A	322	79.122	-19.432	40.251	1.00	25.11
1584	CG	TYR	A	322	79.911	-19.624	41.541	1.00	25.40
1585	CD1	TYR	A	322	81.291	-19.576	41.519	1.00	25.69
1586	CD2	TYR	A	322	79.282	-19.866	42.764	1.00	25.12
1587	CE1	TYR	A	322	82.037	-19.772	42.669	1.00	26.68
1588	CE2	TYR	A	322	80.010	-20.046	43.920	1.00	26.18
1589	CZ	TYR	A	322	81.383	-19.999	43.871	1.00	26.75
1590	OH	TYR	A	322	82.145	-20.197	44.987	1.00	27.96
1591	N	SER	A	323	79.858	-22.517	40.812	1.00	27.80
1592	CA	SER	A	323	79.884	-23.498	41.882	1.00	28.44
1593	C	SER	A	323	81.291	-23.469	42.494	1.00	28.56
1594	O	SER	A	323	82.252	-22.944	41.901	1.00	26.33
1595	CB	SER	A	323	79.467	-24.897	41.536	1.00	27.55
1596	OG	SER	A	323	80.342	-25.551	40.633	1.00	29.60
1597	N	LYS	A	324	81.399	-24.048	43.683	1.00	29.32
1598	CA	LYS	A	324	82.674	-24.064	44.394	1.00	31.61
1599	C	LYS	A	324	83.804	-24.679	43.609	1.00	30.15
1600	O	LYS	A	324	84.882	-24.101	43.574	1.00	29.36
1601	CB	LYS	A	324	82.529	-24.863	45.697	1.00	35.71
1602	CG	LYS	A	324	82.413	-23.989	46.937	1.00	40.11
1603	CD	LYS	A	324	82.177	-24.926	48.134	1.00	42.85
1604	CE	LYS	A	324	80.695	-25.015	48.452	1.00	44.71
1605	NZ	LYS	A	324	80.253	-23.993	49.436	1.00	46.25
1606	N	ASP	A	325	83.595	-25.836	42.979	1.00	30.61
1607	CA	ASP	A	325	84.674	-26.467	42.219	1.00	31.24
1608	C	ASP	A	325	84.934	-25.989	40.810	1.00	30.11
1609	O	ASP	A	325	86.033	-26.273	40.306	1.00	28.10
1610	CB	ASP	A	325	84.425	-27.990	42.162	1.00	34.10
1611	CG	ASP	A	325	84.438	-28.490	43.607	1.00	38.46
1612	OD1	ASP	A	325	85.027	-27.884	44.523	1.00	39.44
1613	OD2	ASP	A	325	83.746	-29.499	43.857	1.00	40.94
1614	N	ALA	A	326	84.007	-25.274	40.168	1.00	26.93
1615	CA	ALA	A	326	84.226	-24.816	38.800	1.00	24.07
1616	C	ALA	A	326	83.169	-23.821	38.324	1.00	23.18
1617	O	ALA	A	326	82.044	-23.822	38.845	1.00	23.26
1618	CB	ALA	A	326	84.066	-26.016	37.844	1.00	25.03
1619	N	THR	A	327	83.521	-23.011	37.326	1.00	22.27
1620	CA	THR	A	327	82.521	-22.114	36.751	1.00	22.23
1621	C	THR	A	327	82.410	-22.371	35.241	1.00	23.00
1622	O	THR	A	327	83.464	-22.441	34.587	1.00	22.16
1623	CB	THR	A	327	82.822	-20.630	36.971	1.00	22.19
1624	OG1	THR	A	327	82.652	-20.444	38.359	1.00	20.51
1625	CG2	THR	A	327	81.815	-19.716	36.226	1.00	21.57
1626	N	SER	A	328	81.189	-22.495	34.728	1.00	20.66
1627	CA	SER	A	328	81.065	-22.697	33.273	1.00	21.04
1628	C	SER	A	328	80.570	-21.437	32.555	1.00	21.82
1629	O	SER	A	328	79.704	-20.724	33.080	1.00	20.39

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1630	CB	SER	A	328	80.013	-23.762	33.010	1.00	22.57
1631	OG	SER	A	328	80.420	-25.021	33.487	1.00	26.12
1632	N	PHE	A	329	81.055	-21.187	31.335	1.00	20.94
1633	CA	PHE	A	329	80.703	-19.990	30.587	1.00	19.32
1634	C	PHE	A	329	80.108	-20.361	29.232	1.00	20.62
1635	O	PHE	A	329	80.520	-21.374	28.618	1.00	18.58
1636	CB	PHE	A	329	81.937	-19.097	30.414	1.00	17.82
1637	CG	PHE	A	329	82.637	-18.648	31.677	1.00	19.59
1638	CD1	PHE	A	329	83.556	-19.478	32.308	1.00	16.87
1639	CD2	PHE	A	329	82.377	-17.385	32.209	1.00	19.26
1640	CE1	PHE	A	329	84.195	-19.074	33.465	1.00	19.15
1641	CE2	PHE	A	329	83.064	-16.954	33.344	1.00	18.66
1642	CZ	PHE	A	329	83.904	-17.819	33.995	1.00	19.30
1643	N	ARG	A	330	79.142	-19.576	28.754	1.00	19.04
1644	CA	ARG	A	330	78.571	-19.791	27.432	1.00	17.97
1645	C	ARG	A	330	78.029	-18.474	26.858	1.00	19.63
1646	O	ARG	A	330	77.319	-17.717	27.557	1.00	18.47
1647	CB	ARG	A	330	77.471	-20.860	27.393	1.00	20.74
1648	CG	ARG	A	330	77.092	-21.262	25.948	1.00	21.20
1649	CD	ARG	A	330	75.983	-22.295	25.893	1.00	21.96
1650	NE	ARG	A	330	76.296	-23.594	26.492	1.00	22.92
1651	CZ	ARG	A	330	76.812	-24.638	25.839	1.00	23.47
1652	NH1	ARG	A	330	77.076	-25.760	26.503	1.00	23.14
1653	NH2	ARG	A	330	77.034	-24.625	24.528	1.00	20.70
1654	N	VAL	A	331	78.421	-18.196	25.605	1.00	18.50
1655	CA	VAL	A	331	77.991	-16.939	24.952	1.00	18.28
1656	C	VAL	A	331	77.605	-17.227	23.505	1.00	17.84
1657	O	VAL	A	331	78.271	-18.081	22.888	1.00	17.02
1658	CB	VAL	A	331	79.103	-15.885	25.030	1.00	17.74
1659	CG1	VAL	A	331	80.369	-16.391	24.320	1.00	18.41
1660	CG2	VAL	A	331	78.693	-14.550	24.422	1.00	18.27
1661	N	TRP	A	332	76.561	-16.576	22.985	1.00	17.30
1662	CA	TRP	A	332	76.128	-16.832	21.606	1.00	16.55
1663	C	TRP	A	332	76.872	-15.925	20.635	1.00	16.29
1664	O	TRP	A	332	76.694	-14.711	20.747	1.00	16.81
1665	CB	TRP	A	332	74.607	-16.801	21.475	1.00	15.95
1666	CG	TRP	A	332	73.976	-17.064	20.126	1.00	16.61
1667	CD1	TRP	A	332	73.873	-18.291	19.532	1.00	16.92
1668	CD2	TRP	A	332	73.332	-16.134	19.237	1.00	16.47
1669	NE1	TRP	A	332	73.231	-18.170	18.311	1.00	18.27
1670	CE2	TRP	A	332	72.866	-16.865	18.119	1.00	17.73
1671	CE3	TRP	A	332	73.178	-14.747	19.217	1.00	16.21
1672	CZ2	TRP	A	332	72.274	-16.256	17.010	1.00	16.41
1673	CZ3	TRP	A	332	72.531	-14.138	18.143	1.00	16.52
1674	CH2	TRP	A	332	72.075	-14.905	17.057	1.00	15.60
1675	N	ALA	A	333	77.714	-16.446	19.737	1.00	16.60
1676	CA	ALA	A	333	78.444	-15.553	18.786	1.00	17.43
1677	C	ALA	A	333	78.657	-16.275	17.466	1.00	17.33
1678	O	ALA	A	333	79.767	-16.726	17.165	1.00	17.44
1679	CB	ALA	A	333	79.803	-15.187	19.395	1.00	17.32
1680	N	PRO	A	334	77.615	-16.422	16.640	1.00	16.81
1681	CA	PRO	A	334	77.667	-17.222	15.426	1.00	16.90
1682	C	PRO	A	334	78.499	-16.717	14.264	1.00	18.01
1683	O	PRO	A	334	78.812	-17.501	13.340	1.00	19.09
1684	CB	PRO	A	334	76.165	-17.379	15.095	1.00	17.28
1685	CG	PRO	A	334	75.567	-16.049	15.533	1.00	17.13
1686	CD	PRO	A	334	76.259	-15.842	16.881	1.00	15.63
1687	N	THR	A	335	78.966	-15.478	14.258	1.00	17.49
1688	CA	THR	A	335	79.765	-14.969	13.145	1.00	19.36
1689	C	THR	A	335	81.245	-14.804	13.484	1.00	19.67
1690	O	THR	A	335	82.095	-14.363	12.681	1.00	19.24
1691	CB	THR	A	335	79.202	-13.632	12.595	1.00	19.04
1692	OG1	THR	A	335	79.459	-12.557	13.518	1.00	18.31
1693	CG2	THR	A	335	77.709	-13.744	12.268	1.00	18.55
1694	N	ALA	A	336	81.589	-15.082	14.737	1.00	20.15
1695	CA	ALA	A	336	82.961	-14.943	15.225	1.00	21.16
1696	C	ALA	A	336	83.915	-16.034	14.731	1.00	20.66
1697	O	ALA	A	336	83.522	-17.199	14.668	1.00	20.80
1698	CB	ALA	A	336	82.965	-15.048	16.765	1.00	19.61
1699	N	SER	A	337	85.164	-15.642	14.454	1.00	21.24
1700	CA	SER	A	337	86.158	-16.646	14.033	1.00	21.72
1701	C	SER	A	337	86.913	-17.153	15.263	1.00	22.44
1702	O	SER	A	337	87.457	-18.262	15.262	1.00	22.33
1703	CB	SER	A	337	87.101	-16.133	12.942	1.00	19.79
1704	OG	SER	A	337	87.842	-15.014	13.378	1.00	19.73
1705	N	ASN	A	338	86.800	-16.461	16.395	1.00	22.39
1706	CA	ASN	A	338	87.474	-16.897	17.629	1.00	22.59
1707	C	ASN	A	338	86.895	-16.133	18.822	1.00	21.70
1708	O	ASN	A	338	86.551	-14.961	18.662	1.00	20.21
1709	CB	ASN	A	338	88.985	-16.546	17.593	1.00	23.25
1710	CG	ASN	A	338	89.769	-17.286	18.665	1.00	23.27
1711	OD1	ASN	A	338	89.309	-18.312	19.176	1.00	24.41
1712	ND2	ASN	A	338	90.949	-16.819	19.009	1.00	22.31
1713	N	VAL	A	339	86.788	-16.750	19.982	1.00	20.64
1714	CA	VAL	A	339	86.296	-16.110	21.195	1.00	20.83
1715	C	VAL	A	339	87.216	-16.633	22.325	1.00	21.76
1716	O	VAL	A	339	87.446	-17.852	22.405	1.00	20.76
1717	CB	VAL	A	339	84.849	-16.455	21.599	1.00	20.75
1718	CG1	VAL	A	339	84.446	-15.701	22.879	1.00	20.39
1719	CG2	VAL	A	339	83.840	-16.157	20.492	1.00	20.29
1720	N	GLN	A	340	87.759	-15.716	23.111	1.00	19.11
1721	CA	GLN	A	340	88.577	-16.086	24.253	1.00	21.95
1722	C	GLN	A	340	87.972	-15.504	25.543	1.00	22.76
1723	O	GLN	A	340	87.332	-14.438	25.536	1.00	20.68
1724	CB	GLN	A	340	90.005	-15.531	24.024	1.00	25.09
1725	CG	GLN	A	340	90.662	-16.091	22.738	1.00	28.48

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1726	CD	GLN	A	340	92.158	-15.840	22.679	1.00	32.41
1727	OE1	GLN	A	340	92.611	-14.980	21.913	1.00	34.76
1728	NE2	GLN	A	340	92.927	-16.566	23.479	1.00	32.06
1729	N	LEU	A	341	88.203	-16.164	26.673	1.00	21.03
1730	CA	LEU	A	341	87.802	-15.701	27.996	1.00	19.98
1731	C	LEU	A	341	88.980	-14.997	28.691	1.00	20.18
1732	O	LEU	A	341	90.067	-15.556	28.788	1.00	18.71
1733	CB	LEU	A	341	87.383	-16.917	28.829	1.00	19.90
1734	CG	LEU	A	341	86.998	-16.678	30.295	1.00	21.43
1735	CD1	LEU	A	341	85.703	-15.837	30.345	1.00	20.84
1736	CD2	LEU	A	341	86.828	-18.018	31.006	1.00	20.08
1737	N	LEU	A	342	88.796	-13.750	29.074	1.00	19.42
1738	CA	LEU	A	342	89.731	-12.963	29.842	1.00	21.69
1739	C	LEU	A	342	89.252	-12.963	31.306	1.00	22.85
1740	O	LEU	A	342	88.125	-12.555	31.641	1.00	21.27
1741	CB	LEU	A	342	89.901	-11.557	29.277	1.00	22.45
1742	CG	LEU	A	342	90.120	-11.437	27.750	1.00	23.01
1743	CD1	LEU	A	342	90.324	-9.977	27.354	1.00	20.48
1744	CD2	LEU	A	342	91.270	-12.283	27.239	1.00	24.22
1745	N	LEU	A	343	90.090	-13.551	32.167	1.00	21.42
1746	CA	LEU	A	343	89.834	-13.675	33.594	1.00	22.82
1747	C	LEU	A	343	90.771	-12.755	34.359	1.00	23.56
1748	O	LEU	A	343	91.973	-12.618	34.049	1.00	22.34
1749	CB	LEU	A	343	89.977	-15.095	34.112	1.00	23.13
1750	CG	LEU	A	343	88.936	-16.134	33.765	1.00	24.04
1751	CD1	LEU	A	343	89.386	-17.523	34.242	1.00	22.59
1752	CD2	LEU	A	343	87.574	-15.819	34.402	1.00	22.28
1753	N	TYR	A	344	90.187	-12.001	35.296	1.00	21.67
1754	CA	TYR	A	344	90.891	-11.029	36.081	1.00	20.84
1755	C	TYR	A	344	90.731	-11.309	37.578	1.00	22.98
1756	O	TYR	A	344	89.595	-11.488	38.042	1.00	20.73
1757	CB	TYR	A	344	90.471	-9.590	35.781	1.00	22.01
1758	CG	TYR	A	344	90.514	-9.119	34.350	1.00	22.91
1759	CD1	TYR	A	344	89.464	-9.443	33.473	1.00	23.47
1760	CD2	TYR	A	344	91.589	-8.413	33.839	1.00	23.31
1761	CE1	TYR	A	344	89.503	-9.068	32.134	1.00	22.88
1762	CE2	TYR	A	344	91.600	-7.977	32.516	1.00	24.05
1763	CZ	TYR	A	344	90.574	-8.343	31.665	1.00	23.45
1764	OH	TYR	A	344	90.607	-7.928	30.344	1.00	21.39
1765	N	ASN	A	345	91.843	-11.311	38.344	1.00	23.99
1766	CA	ASN	A	345	91.708	-11.557	39.793	1.00	26.27
1767	C	ASN	A	345	91.603	-10.255	40.558	1.00	26.36
1768	O	ASN	A	345	91.850	-10.193	41.752	1.00	28.06
1769	CB	ASN	A	345	92.841	-12.427	40.366	1.00	27.33
1770	CG	ASN	A	345	94.204	-11.783	40.253	1.00	27.96
1771	OD1	ASN	A	345	94.333	-10.580	39.995	1.00	26.96
1772	ND2	ASN	A	345	95.254	-12.588	40.461	1.00	30.19
1773	N	SER	A	346	91.183	-9.172	39.904	1.00	27.11
1774	CA	SER	A	346	91.040	-7.885	40.569	1.00	26.45
1775	C	SER	A	346	90.101	-7.018	39.745	1.00	26.06
1776	O	SER	A	346	89.895	-7.299	38.564	1.00	26.29
1777	CB	SER	A	346	92.413	-7.241	40.740	1.00	24.63
1778	OG	SER	A	346	92.769	-6.551	39.569	1.00	23.97
1779	N	GLU	A	347	89.587	-5.953	40.320	1.00	25.01
1780	CA	GLU	A	347	88.629	-5.103	39.610	1.00	26.48
1781	C	GLU	A	347	89.285	-4.207	38.593	1.00	27.56
1782	O	GLU	A	347	88.618	-3.846	37.608	1.00	26.07
1783	CB	GLU	A	347	87.833	-4.290	40.665	1.00	26.52
1784	CG	GLU	A	347	86.563	-3.647	40.158	1.00	25.42
1785	CD	GLU	A	347	85.681	-3.082	41.265	1.00	25.59
1786	OE1	GLU	A	347	84.477	-2.829	41.018	1.00	23.17
1787	OE2	GLU	A	347	86.140	-2.884	42.416	1.00	24.63
1788	N	LYS	A	348	90.532	-3.758	38.843	1.00	27.94
1789	CA	LYS	A	348	91.239	-2.907	37.892	1.00	30.23
1790	C	LYS	A	348	92.602	-3.443	37.434	1.00	30.18
1791	O	LYS	A	348	93.183	-2.871	36.515	1.00	30.31
1792	CB	LYS	A	348	91.496	-1.484	38.403	1.00	32.74
1793	CG	LYS	A	348	90.350	-0.740	39.058	1.00	36.60
1794	CD	LYS	A	348	90.397	-0.890	40.579	1.00	39.69
1795	CE	LYS	A	348	91.755	-0.453	41.157	1.00	40.78
1796	NZ	LYS	A	348	91.956	-0.820	42.572	1.00	40.05
1797	N	GLY	A	349	93.121	-4.508	38.002	1.00	29.40
1798	CA	GLY	A	349	94.413	-5.069	37.659	1.00	30.15
1799	C	GLY	A	349	94.469	-5.699	36.268	1.00	29.96
1800	O	GLY	A	349	93.436	-5.955	35.630	1.00	26.44
1801	N	SER	A	350	95.695	-5.979	35.812	1.00	27.06
1802	CA	SER	A	350	95.884	-6.505	34.472	1.00	26.80
1803	C	SER	A	350	95.470	-7.962	34.377	1.00	27.11
1804	O	SER	A	350	95.237	-8.656	35.366	1.00	26.51
1805	CB	SER	A	350	97.333	-6.250	33.997	1.00	28.64
1806	OG	SER	A	350	98.234	-7.164	34.581	1.00	25.07
1807	N	ILE	A	351	95.238	-8.418	33.148	1.00	27.83
1808	CA	ILE	A	351	94.751	-9.754	32.873	1.00	27.61
1809	C	ILE	A	351	95.544	-10.819	33.604	1.00	28.09
1810	O	ILE	A	351	96.782	-10.849	33.632	1.00	25.86
1811	CB	ILE	A	351	94.698	-10.042	31.362	1.00	30.70
1812	CG1	ILE	A	351	94.270	-11.501	31.097	1.00	30.30
1813	CG2	ILE	A	351	96.082	-9.848	30.749	1.00	32.44
1814	CD1	ILE	A	351	93.598	-11.582	29.747	1.00	33.45
1815	N	THR	A	352	94.804	-11.747	34.211	1.00	26.74
1816	CA	THR	A	352	95.382	-12.823	34.980	1.00	27.48
1817	C	THR	A	352	95.555	-14.073	34.136	1.00	28.86
1818	O	THR	A	352	96.539	-14.780	34.332	1.00	29.06
1819	CB	THR	A	352	94.507	-13.196	36.212	1.00	26.13
1820	OG1	THR	A	352	94.336	-11.981	36.927	1.00	25.38
1821	CG2	THR	A	352	95.178	-14.198	37.140	1.00	27.23

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1822	N	LYS	A	353	94.575	-14.379	33.308	1.00	28.99
1823	CA	LYS	A	353	94.536	-15.603	32.517	1.00	31.07
1824	C	LYS	A	353	93.738	-15.337	31.224	1.00	31.82
1825	O	LYS	A	353	92.623	-14.771	31.223	1.00	26.80
1826	CB	LYS	A	353	93.848	-16.644	33.383	1.00	34.73
1827	CG	LYS	A	353	94.468	-17.997	33.598	1.00	40.91
1828	CD	LYS	A	353	93.462	-19.025	34.085	1.00	44.90
1829	CE	LYS	A	353	93.470	-19.297	35.585	1.00	47.03
1830	NZ	LYS	A	353	92.210	-20.014	35.986	1.00	47.57
1831	N	GLN	A	354	94.323	-15.729	30.091	1.00	29.04
1832	CA	GLN	A	354	93.676	-15.609	28.795	1.00	29.05
1833	C	GLN	A	354	93.487	-17.017	28.238	1.00	30.10
1834	O	GLN	A	354	94.488	-17.758	28.103	1.00	31.21
1835	CB	GLN	A	354	94.467	-14.688	27.880	1.00	29.18
1836	CG	GLN	A	354	93.905	-14.566	26.477	1.00	31.51
1837	CD	GLN	A	354	94.412	-13.380	25.699	1.00	35.08
1838	OE1	GLN	A	354	94.375	-13.338	24.466	1.00	37.15
1839	NE2	GLN	A	354	94.905	-12.320	26.329	1.00	37.06
1840	N	LEU	A	355	92.253	-17.454	28.014	1.00	25.86
1841	CA	LEU	A	355	91.935	-18.815	27.630	1.00	25.52
1842	C	LEU	A	355	91.099	-18.933	26.358	1.00	25.60
1843	O	LEU	A	355	90.052	-18.276	26.296	1.00	23.63
1844	CB	LEU	A	355	91.104	-19.459	28.763	1.00	23.98
1845	CG	LEU	A	355	91.678	-20.180	29.957	1.00	27.14
1846	CD1	LEU	A	355	93.202	-20.110	30.090	1.00	24.35
1847	CD2	LEU	A	355	91.046	-19.801	31.294	1.00	24.19
1848	N	GLU	A	356	91.388	-19.914	25.498	1.00	24.90
1849	CA	GLU	A	356	90.561	-20.149	24.328	1.00	25.07
1850	C	GLU	A	356	89.240	-20.795	24.749	1.00	24.27
1851	O	GLU	A	356	89.220	-21.728	25.556	1.00	24.57
1852	CB	GLU	A	356	91.263	-21.110	23.354	1.00	26.34
1853	CG	GLU	A	356	92.307	-20.425	22.486	1.00	28.70
1854	CD	GLU	A	356	91.664	-19.583	21.391	1.00	29.91
1855	OE1	GLU	A	356	90.508	-19.768	20.973	1.00	30.84
1856	OE2	GLU	A	356	92.360	-18.651	20.957	1.00	31.88
1857	N	MET	A	357	88.138	-20.398	24.144	1.00	24.03
1858	CA	MET	A	357	86.839	-21.025	24.390	1.00	21.73
1859	C	MET	A	357	86.645	-22.023	23.268	1.00	22.56
1860	O	MET	A	357	87.422	-21.932	22.306	1.00	23.10
1861	CB	MET	A	357	85.724	-19.974	24.468	1.00	20.62
1862	CG	MET	A	357	85.893	-19.016	25.636	1.00	19.78
1863	SD	MET	A	357	84.518	-17.881	25.954	1.00	18.56
1864	CE	MET	A	357	83.209	-19.002	26.424	1.00	17.50
1865	N	GLN	A	358	85.749	-22.969	23.351	1.00	23.45
1866	CA	GLN	A	358	85.504	-23.939	22.312	1.00	26.55
1867	C	GLN	A	358	84.150	-23.684	21.603	1.00	25.08
1868	O	GLN	A	358	83.110	-23.528	22.253	1.00	21.83
1869	CB	GLN	A	358	85.324	-25.373	22.847	1.00	29.06
1870	CG	GLN	A	358	85.931	-25.673	24.194	1.00	36.05
1871	CD	GLN	A	358	85.318	-26.928	24.804	1.00	38.87
1872	OE1	GLN	A	358	85.386	-27.019	26.035	1.00	42.36
1873	NE2	GLN	A	358	84.727	-27.807	23.987	1.00	40.44
1874	N	LYS	A	359	84.197	-23.798	20.304	1.00	24.04
1875	CA	LYS	A	359	83.007	-23.709	19.465	1.00	26.25
1876	C	LYS	A	359	82.043	-24.816	19.852	1.00	24.84
1877	O	LYS	A	359	82.493	-25.956	19.974	1.00	26.59
1878	CB	LYS	A	359	83.343	-23.834	17.978	1.00	26.51
1879	CG	LYS	A	359	82.110	-23.602	17.112	1.00	29.91
1880	CD	LYS	A	359	81.361	-22.329	17.504	1.00	30.23
1881	CE	LYS	A	359	79.954	-22.267	16.933	1.00	28.64
1882	NZ	LYS	A	359	80.031	-22.364	15.441	1.00	28.49
1883	N	SER	A	360	80.782	-24.516	20.104	1.00	23.90
1884	CA	SER	A	360	79.794	-25.489	20.549	1.00	23.71
1885	C	SER	A	360	78.515	-25.385	19.738	1.00	24.86
1886	O	SER	A	360	78.513	-24.861	18.608	1.00	23.35
1887	CB	SER	A	360	79.587	-25.315	22.070	1.00	23.14
1888	OG	SER	A	360	78.641	-26.216	22.656	1.00	22.35
1889	N	ASP	A	361	77.405	-25.945	20.249	1.00	23.82
1890	CA	ASP	A	361	76.173	-25.979	19.475	1.00	25.63
1891	C	ASP	A	361	75.582	-24.625	19.066	1.00	23.92
1892	O	ASP	A	361	75.515	-23.693	19.861	1.00	21.92
1893	CB	ASP	A	361	75.057	-26.676	20.281	1.00	29.13
1894	CG	ASP	A	361	75.440	-28.089	20.700	1.00	33.65
1895	OD1	ASP	A	361	76.245	-28.789	20.062	1.00	34.34
1896	OD2	ASP	A	361	74.868	-28.505	21.735	1.00	37.02
1897	N	ASN	A	362	74.897	-24.624	17.935	1.00	22.19
1898	CA	ASN	A	362	74.108	-23.504	17.439	1.00	20.84
1899	C	ASN	A	362	74.723	-22.135	17.566	1.00	20.78
1900	O	ASN	A	362	74.034	-21.188	18.003	1.00	22.45
1901	CB	ASN	A	362	72.734	-23.521	18.149	1.00	21.03
1902	CG	ASN	A	362	72.027	-24.871	18.007	1.00	21.03
1903	OD1	ASN	A	362	71.503	-25.284	16.951	1.00	20.90
1904	ND2	ASN	A	362	71.904	-25.578	19.095	1.00	17.27
1905	N	GLY	A	363	75.986	-21.960	17.142	1.00	19.74
1906	CA	GLY	A	363	76.621	-20.650	17.206	1.00	18.96
1907	C	GLY	A	363	77.260	-20.272	18.543	1.00	18.21
1908	O	GLY	A	363	77.931	-19.229	18.591	1.00	15.89
1909	N	THR	A	364	77.156	-21.080	19.578	1.00	15.00
1910	CA	THR	A	364	77.689	-20.699	20.880	1.00	17.37
1911	C	THR	A	364	79.156	-21.147	21.019	1.00	17.64
1912	O	THR	A	364	79.666	-21.891	20.195	1.00	17.37
1913	CB	THR	A	364	76.957	-21.274	22.108	1.00	17.36
1914	OG1	THR	A	364	76.996	-22.715	22.132	1.00	18.13
1915	CG2	THR	A	364	75.462	-20.902	22.195	1.00	18.48
1916	N	TRP	A	365	79.861	-20.549	21.955	1.00	17.83
1917	CA	TRP	A	365	81.196	-20.835	22.405	1.00	20.62

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1918	C	TRP	A	365	81.074	-21.135	23.903	1.00	22.44
1919	O	TRP	A	365	80.263	-20.458	24.568	1.00	22.38
1920	CB	TRP	A	365	82.167	-19.660	22.183	1.00	19.73
1921	CG	TRP	A	365	82.409	-19.420	20.718	1.00	20.76
1922	CD1	TRP	A	365	81.510	-18.888	19.822	1.00	19.99
1923	CD2	TRP	A	365	83.597	-19.712	19.980	1.00	20.44
1924	NE1	TRP	A	365	82.068	-18.850	18.572	1.00	20.24
1925	CE2	TRP	A	365	83.351	-19.360	18.646	1.00	21.78
1926	CE3	TRP	A	365	84.852	-20.236	20.320	1.00	22.22
1927	CZ2	TRP	A	365	84.325	-19.484	17.645	1.00	21.66
1928	CZ3	TRP	A	365	85.821	-20.393	19.335	1.00	22.86
1929	CH2	TRP	A	365	85.540	-20.011	18.007	1.00	23.02
1930	N	LYS	A	366	81.789	-22.120	24.428	1.00	22.80
1931	CA	LYS	A	366	81.671	-22.479	25.839	1.00	23.01
1932	C	LYS	A	366	83.034	-22.735	26.462	1.00	24.27
1933	O	LYS	A	366	84.052	-22.851	25.763	1.00	22.69
1934	CB	LYS	A	366	80.802	-23.755	25.943	1.00	23.05
1935	CG	LYS	A	366	81.567	-25.016	25.499	1.00	23.62
1936	CD	LYS	A	366	80.702	-26.253	25.725	1.00	25.72
1937	CE	LYS	A	366	81.449	-27.535	25.340	1.00	28.42
1938	NZ	LYS	A	366	80.483	-28.675	25.518	1.00	30.63
1939	N	LEU	A	367	83.102	-22.838	27.785	1.00	24.03
1940	CA	LEU	A	367	84.359	-23.148	28.478	1.00	23.96
1941	C	LEU	A	367	84.084	-23.398	29.967	1.00	25.05
1942	O	LEU	A	367	83.301	-22.711	30.631	1.00	20.92
1943	CB	LEU	A	367	85.480	-22.129	28.320	1.00	24.83
1944	CG	LEU	A	367	86.823	-22.510	28.968	1.00	24.39
1945	CD1	LEU	A	367	87.419	-23.727	28.264	1.00	24.41
1946	CD2	LEU	A	367	87.859	-21.399	28.947	1.00	22.93
1947	N	GLN	A	368	84.576	-24.553	30.440	1.00	26.14
1948	CA	GLN	A	368	84.447	-24.893	31.849	1.00	27.03
1949	C	GLN	A	368	85.791	-24.611	32.529	1.00	26.26
1950	O	GLN	A	368	86.816	-25.102	32.007	1.00	23.19
1951	CB	GLN	A	368	84.045	-26.354	32.059	1.00	29.88
1952	CG	GLN	A	368	83.942	-26.621	33.557	1.00	34.12
1953	CD	GLN	A	368	83.326	-27.947	33.888	1.00	38.21
1954	OE1	GLN	A	368	82.163	-28.268	33.661	1.00	41.75
1955	NE2	GLN	A	368	84.076	-28.846	34.488	1.00	39.92
1956	N	VAL	A	369	85.811	-23.779	33.570	1.00	25.22
1957	CA	VAL	A	369	87.072	-23.466	34.227	1.00	26.94
1958	C	VAL	A	369	87.104	-24.075	35.641	1.00	27.56
1959	O	VAL	A	369	86.251	-23.711	36.453	1.00	26.74
1960	CB	VAL	A	369	87.404	-21.975	34.403	1.00	27.02
1961	CG1	VAL	A	369	88.793	-21.803	35.043	1.00	28.37
1962	CG2	VAL	A	369	87.375	-21.200	33.086	1.00	26.62
1963	N	SER	A	370	88.133	-24.863	35.929	1.00	27.55
1964	CA	SER	A	370	88.332	-25.436	37.261	1.00	30.11
1965	C	SER	A	370	88.809	-24.485	38.333	1.00	27.75
1966	O	SER	A	370	89.579	-23.573	38.078	1.00	28.00
1967	CB	SER	A	370	89.397	-26.574	37.177	1.00	31.50
1968	OG	SER	A	370	88.799	-27.545	36.318	1.00	35.78
1969	N	GLY	A	371	88.380	-24.676	39.577	1.00	31.30
1970	CA	GLY	A	371	88.784	-23.771	40.670	1.00	30.93
1971	C	GLY	A	371	87.571	-22.927	41.091	1.00	32.19
1972	O	GLY	A	371	86.518	-22.988	40.453	1.00	30.29
1973	N	ASN	A	372	87.725	-22.211	42.194	1.00	31.23
1974	CA	ASN	A	372	86.626	-21.395	42.752	1.00	31.68
1975	C	ASN	A	372	86.774	-19.969	42.243	1.00	28.25
1976	O	ASN	A	372	87.724	-19.265	42.643	1.00	28.03
1977	CB	ASN	A	372	86.716	-21.406	44.286	1.00	33.96
1978	CG	ASN	A	372	85.534	-20.773	44.992	1.00	36.29
1979	OD1	ASN	A	372	84.864	-19.865	44.493	1.00	35.90
1980	ND2	ASN	A	372	85.211	-21.241	46.212	1.00	35.53
1981	N	LEU	A	373	85.865	-19.526	41.377	1.00	25.26
1982	CA	LEU	A	373	86.006	-18.204	40.775	1.00	23.40
1983	C	LEU	A	373	85.148	-17.151	41.456	1.00	22.75
1984	O	LEU	A	373	84.924	-16.071	40.902	1.00	20.78
1985	CB	LEU	A	373	85.754	-18.243	39.260	1.00	23.70
1986	CG	LEU	A	373	86.733	-19.077	38.413	1.00	24.26
1987	CD1	LEU	A	373	86.538	-18.827	36.918	1.00	24.86
1988	CD2	LEU	A	373	88.185	-18.745	38.729	1.00	26.18
1989	N	GLU	A	374	84.705	-17.422	42.691	1.00	22.76
1990	CA	GLU	A	374	83.955	-16.376	43.386	1.00	20.88
1991	C	GLU	A	374	84.658	-15.013	43.353	1.00	21.01
1992	O	GLU	A	374	85.868	-14.894	43.493	1.00	18.90
1993	CB	GLU	A	374	83.722	-16.806	44.835	1.00	23.51
1994	CG	GLU	A	374	82.766	-15.862	45.565	1.00	25.57
1995	CD	GLU	A	374	82.144	-16.577	46.741	1.00	29.28
1996	OE1	GLU	A	374	82.604	-17.657	47.084	1.00	29.30
1997	OE2	GLU	A	374	81.193	-16.042	47.307	1.00	27.72
1998	N	ASN	A	375	83.841	-13.965	43.118	1.00	19.21
1999	CA	ASN	A	375	84.357	-12.596	43.101	1.00	19.30
2000	C	ASN	A	375	85.512	-12.400	42.116	1.00	19.99
2001	O	ASN	A	375	86.381	-11.553	42.288	1.00	18.96
2002	CB	ASN	A	375	84.810	-12.224	44.515	1.00	21.23
2003	CG	ASN	A	375	83.658	-12.390	45.469	1.00	22.98
2004	OD1	ASN	A	375	83.828	-12.711	46.642	1.00	21.72
2005	ND2	ASN	A	375	82.446	-12.157	44.937	1.00	19.08
2006	N	TRP	A	376	85.534	-13.250	41.077	1.00	18.63
2007	CA	TRP	A	376	86.479	-13.023	39.991	1.00	20.31
2008	C	TRP	A	376	85.908	-12.050	38.948	1.00	20.90
2009	O	TRP	A	376	84.705	-11.885	38.809	1.00	20.95
2010	CB	TRP	A	376	86.796	-14.374	39.348	1.00	21.71
2011	CG	TRP	A	376	87.964	-15.000	40.012	1.00	22.49
2012	CD1	TRP	A	376	88.036	-15.457	41.347	1.00	20.13
2013	CD2	TRP	A	376	89.290	-15.156	39.450	1.00	22.92

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2014	NE1	TRP	A	376	89.280	-15.887	41.683	1.00	20.87
2015	CE2	TRP	A	376	90.116	-15.690	40.471	1.00	22.98
2016	CE3	TRP	A	376	89.839	-14.871	38.203	1.00	23.59
2017	CZ2	TRP	A	376	91.464	-15.903	40.230	1.00	23.06
2018	CZ3	TRP	A	376	91.187	-15.088	37.962	1.00	24.45
2019	CH2	TRP	A	376	92.005	-15.606	38.983	1.00	23.52
2020	N	TYR	A	377	86.618	-11.303	38.111	1.00	19.49
2021	CA	TYR	A	377	86.016	-10.505	37.051	1.00	19.50
2022	C	TYR	A	377	86.358	-11.145	35.703	1.00	20.68
2023	O	TYR	A	377	87.330	-11.914	35.605	1.00	19.41
2024	CB	TYR	A	377	86.409	-9.027	37.144	1.00	17.91
2025	CG	TYR	A	377	85.956	-8.348	38.427	1.00	18.83
2026	CD1	TYR	A	377	86.708	-8.461	39.604	1.00	19.72
2027	CD2	TYR	A	377	84.808	-7.586	38.514	1.00	17.93
2028	CE1	TYR	A	377	86.334	-7.877	40.796	1.00	18.37
2029	CE2	TYR	A	377	84.394	-6.978	39.692	1.00	17.34
2030	CZ	TYR	A	377	85.181	-7.130	40.849	1.00	20.22
2031	OH	TYR	A	377	84.783	-6.517	42.039	1.00	15.40
2032	N	TYR	A	378	85.628	-10.823	34.626	1.00	20.04
2033	CA	TYR	A	378	85.785	-11.425	33.337	1.00	19.08
2034	C	TYR	A	378	85.235	-10.613	32.166	1.00	19.99
2035	O	TYR	A	378	84.354	-9.760	32.334	1.00	20.17
2036	CB	TYR	A	378	85.171	-12.819	33.281	1.00	18.87
2037	CG	TYR	A	378	83.675	-13.049	33.109	1.00	19.44
2038	CD1	TYR	A	378	83.148	-13.529	31.906	1.00	17.38
2039	CD2	TYR	A	378	82.794	-12.845	34.175	1.00	17.88
2040	CE1	TYR	A	378	81.784	-13.770	31.768	1.00	18.82
2041	CE2	TYR	A	378	81.431	-13.071	34.036	1.00	18.35
2042	CZ	TYR	A	378	80.926	-13.553	32.837	1.00	17.91
2043	OH	TYR	A	378	79.558	-13.797	32.732	1.00	18.43
2044	N	LEU	A	379	85.839	-10.897	30.993	1.00	17.82
2045	CA	LEU	A	379	85.409	-10.274	29.738	1.00	17.08
2046	C	LEU	A	379	85.510	-11.341	28.635	1.00	18.66
2047	O	LEU	A	379	86.145	-12.370	28.873	1.00	15.93
2048	CB	LEU	A	379	86.246	-9.088	29.300	1.00	17.38
2049	CG	LEU	A	379	86.193	-7.747	30.010	1.00	19.69
2050	CD1	LEU	A	379	87.317	-6.812	29.589	1.00	16.36
2051	CD2	LEU	A	379	84.837	-7.062	29.750	1.00	18.77
2052	N	TYR	A	380	84.730	-11.180	27.547	1.00	19.37
2053	CA	TYR	A	380	84.862	-12.039	26.387	1.00	19.03
2054	C	TYR	A	380	85.691	-11.243	25.346	1.00	19.03
2055	O	TYR	A	380	85.468	-10.031	25.169	1.00	20.13
2056	CB	TYR	A	380	83.558	-12.495	25.715	1.00	17.35
2057	CG	TYR	A	380	82.665	-13.391	26.562	1.00	17.93
2058	CD1	TYR	A	380	81.332	-13.060	26.782	1.00	17.57
2059	CD2	TYR	A	380	83.146	-14.541	27.170	1.00	16.75
2060	CE1	TYR	A	380	80.485	-13.866	27.548	1.00	18.52
2061	CE2	TYR	A	380	82.344	-15.343	27.948	1.00	17.90
2062	CZ	TYR	A	380	81.011	-15.013	28.134	1.00	17.98
2063	OH	TYR	A	380	80.229	-15.823	28.913	1.00	16.91
2064	N	GLN	A	381	86.621	-11.910	24.682	1.00	18.61
2065	CA	GLN	A	381	87.401	-11.198	23.645	1.00	19.39
2066	C	GLN	A	381	86.998	-11.824	22.307	1.00	17.85
2067	O	GLN	A	381	87.207	-13.010	22.046	1.00	17.98
2068	CB	GLN	A	381	88.897	-11.285	23.867	1.00	19.69
2069	CG	GLN	A	381	89.727	-10.637	22.755	1.00	22.60
2070	CD	GLN	A	381	91.215	-10.720	23.077	1.00	26.02
2071	OE1	GLN	A	381	91.901	-11.578	22.528	1.00	29.96
2072	NE2	GLN	A	381	91.773	-9.888	23.933	1.00	24.48
2073	N	VAL	A	382	86.238	-11.084	21.522	1.00	16.71
2074	CA	VAL	A	382	85.570	-11.634	20.346	1.00	16.94
2075	C	VAL	A	382	86.212	-11.103	19.051	1.00	17.81
2076	O	VAL	A	382	86.315	-9.892	18.865	1.00	17.01
2077	CB	VAL	A	382	84.070	-11.250	20.358	1.00	17.30
2078	CG1	VAL	A	382	83.329	-11.902	19.195	1.00	15.09
2079	CG2	VAL	A	382	83.383	-11.617	21.704	1.00	15.18
2080	N	THR	A	383	86.582	-12.029	18.170	1.00	17.62
2081	CA	THR	A	383	87.183	-11.717	16.889	1.00	18.58
2082	C	THR	A	383	86.147	-11.913	15.773	1.00	20.31
2083	O	THR	A	383	85.654	-13.000	15.528	1.00	20.06
2084	CB	THR	A	383	88.445	-12.526	16.483	1.00	15.89
2085	OG1	THR	A	383	89.447	-12.219	17.481	1.00	16.62
2086	CG2	THR	A	383	89.035	-12.075	15.135	1.00	16.58
2087	N	VAL	A	384	85.721	-10.804	15.246	1.00	22.99
2088	CA	VAL	A	384	84.757	-10.704	14.157	1.00	29.90
2089	C	VAL	A	384	85.220	-10.119	12.820	1.00	33.88
2090	O	VAL	A	384	85.356	-8.914	12.654	1.00	35.70
2091	CB	VAL	A	384	83.363	-10.325	14.691	1.00	30.03
2092	CG1	VAL	A	384	82.464	-10.504	13.470	1.00	29.72
2093	CG2	VAL	A	384	82.691	-10.944	15.902	1.00	28.84
2094	N	ASN	A	385	85.449	-11.060	11.887	1.00	20.00
2095	CA	ASN	A	385	85.893	-10.615	10.580	1.00	20.00
2096	C	ASN	A	385	87.128	-9.723	10.723	1.00	20.00
2097	O	ASN	A	385	87.146	-8.572	10.307	1.00	20.00
2098	CB	ASN	A	385	84.918	-10.260	9.442	1.00	20.00
2099	CG	ASN	A	385	85.367	-9.925	8.043	1.00	20.00
2100	OD1	ASN	A	385	86.415	-10.419	7.638	1.00	20.00
2101	ND2	ASN	A	385	84.535	-9.219	7.259	1.00	20.00
2102	N	GLY	A	386	88.171	-10.355	11.286	1.00	20.00
2103	CA	GLY	A	386	89.376	-9.584	11.526	1.00	20.00
2104	C	GLY	A	386	89.506	-8.487	12.584	1.00	20.00
2105	O	GLY	A	386	90.579	-7.957	12.839	1.00	20.00
2106	N	THR	A	387	88.331	-8.168	13.157	1.00	38.04
2107	CA	THR	A	387	88.344	-7.159	14.198	1.00	34.81
2108	C	THR	A	387	87.955	-7.470	15.656	1.00	29.35
2109	O	THR	A	387	86.789	-7.590	16.010	1.00	25.60

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2110	CB	THR	A	387	87.528	-5.883	13.919	1.00	35.26
2111	OG1	THR	A	387	88.115	-5.484	12.678	1.00	38.62
2112	CG2	THR	A	387	87.395	-4.652	14.820	1.00	35.18
2113	N	THR	A	388	88.985	-7.660	16.494	1.00	25.85
2114	CA	THR	A	388	88.710	-8.130	17.839	1.00	22.57
2115	C	THR	A	388	88.537	-6.958	18.802	1.00	23.19
2116	O	THR	A	388	89.230	-5.952	18.738	1.00	19.61
2117	CB	THR	A	388	89.885	-9.000	18.298	1.00	23.33
2118	OG1	THR	A	388	90.119	-10.030	17.334	1.00	21.46
2119	CG2	THR	A	388	89.580	-9.641	19.654	1.00	22.30
2120	N	GLN	A	389	87.527	-7.200	19.658	1.00	22.43
2121	CA	GLN	A	389	87.071	-6.338	20.720	1.00	22.51
2122	C	GLN	A	389	86.719	-7.159	21.964	1.00	20.76
2123	O	GLN	A	389	86.488	-8.371	21.900	1.00	19.22
2124	CB	GLN	A	389	85.816	-5.511	20.338	1.00	24.03
2125	CG	GLN	A	389	85.997	-4.637	19.092	1.00	24.14
2126	CD	GLN	A	389	84.826	-3.772	18.742	1.00	25.61
2127	OE1	GLN	A	389	84.635	-2.750	19.381	1.00	25.60
2128	NE2	GLN	A	389	83.968	-4.122	17.762	1.00	26.31
2129	N	THR	A	390	86.593	-6.495	23.107	1.00	20.02
2130	CA	THR	A	390	86.149	-7.117	24.347	1.00	17.35
2131	C	THR	A	390	84.749	-6.591	24.716	1.00	18.81
2132	O	THR	A	390	84.358	-5.465	24.384	1.00	17.69
2133	CB	THR	A	390	87.071	-6.834	25.557	1.00	17.85
2134	OG1	THR	A	390	87.007	-5.414	25.809	1.00	18.20
2135	CG2	THR	A	390	88.505	-7.265	25.256	1.00	17.70
2136	N	ALA	A	391	84.004	-7.388	25.445	1.00	17.61
2137	CA	ALA	A	391	82.657	-7.095	25.890	1.00	18.43
2138	C	ALA	A	391	82.254	-7.783	27.192	1.00	17.62
2139	O	ALA	A	391	82.712	-8.896	27.470	1.00	17.18
2140	CB	ALA	A	391	81.673	-7.613	24.811	1.00	16.39
2141	N	VAL	A	392	81.382	-7.128	27.942	1.00	17.34
2142	CA	VAL	A	392	80.822	-7.676	29.180	1.00	15.98
2143	C	VAL	A	392	79.722	-8.661	28.776	1.00	15.84
2144	O	VAL	A	392	79.002	-8.376	27.793	1.00	16.85
2145	CB	VAL	A	392	80.205	-6.584	30.070	1.00	15.95
2146	CG1	VAL	A	392	79.490	-7.180	31.301	1.00	15.89
2147	CG2	VAL	A	392	81.266	-5.543	30.482	1.00	15.39
2148	N	ASP	A	393	79.650	-9.799	29.422	1.00	15.45
2149	CA	ASP	A	393	78.587	-10.790	29.162	1.00	16.16
2150	C	ASP	A	393	77.217	-10.175	29.367	1.00	15.39
2151	O	ASP	A	393	76.864	-9.706	30.471	1.00	14.42
2152	CB	ASP	A	393	78.802	-11.946	30.158	1.00	14.87
2153	CG	ASP	A	393	78.031	-13.211	29.948	1.00	16.08
2154	OD1	ASP	A	393	78.506	-14.295	30.403	1.00	16.54
2155	OD2	ASP	A	393	76.950	-13.261	29.285	1.00	17.16
2156	N	PRO	A	394	76.340	-10.247	28.378	1.00	16.89
2157	CA	PRO	A	394	74.976	-9.706	28.510	1.00	18.08
2158	C	PRO	A	394	74.160	-10.345	29.626	1.00	17.40
2159	O	PRO	A	394	73.183	-9.757	30.116	1.00	17.22
2160	CB	PRO	A	394	74.341	-9.948	27.148	1.00	16.39
2161	CG	PRO	A	394	75.545	-9.916	26.223	1.00	18.52
2162	CD	PRO	A	394	76.619	-10.675	26.975	1.00	17.04
2163	N	TYR	A	395	74.517	-11.568	30.006	1.00	16.37
2164	CA	TYR	A	395	73.877	-12.321	31.086	1.00	16.64
2165	C	TYR	A	395	74.578	-12.142	32.436	1.00	16.49
2166	O	TYR	A	395	74.184	-12.763	33.421	1.00	15.61
2167	CB	TYR	A	395	73.809	-13.820	30.721	1.00	16.31
2168	CG	TYR	A	395	72.739	-14.174	29.709	1.00	14.68
2169	CD1	TYR	A	395	71.590	-14.846	30.151	1.00	16.46
2170	CD2	TYR	A	395	72.836	-13.828	28.360	1.00	14.83
2171	CE1	TYR	A	395	70.576	-15.175	29.276	1.00	13.85
2172	CE2	TYR	A	395	71.820	-14.169	27.441	1.00	14.80
2173	CZ	TYR	A	395	70.691	-14.792	27.935	1.00	15.21
2174	OH	TYR	A	395	69.637	-15.146	27.113	1.00	15.56
2175	N	ALA	A	396	75.632	-11.307	32.568	1.00	16.64
2176	CA	ALA	A	396	76.260	-11.116	33.880	1.00	17.32
2177	C	ALA	A	396	75.211	-10.694	34.933	1.00	18.30
2178	O	ALA	A	396	74.298	-9.914	34.629	1.00	15.51
2179	CB	ALA	A	396	77.260	-9.939	33.770	1.00	17.84
2180	N	ARG	A	397	75.388	-11.057	36.198	1.00	16.48
2181	CA	ARG	A	397	74.538	-10.729	37.300	1.00	15.87
2182	C	ARG	A	397	75.103	-9.694	38.274	1.00	18.12
2183	O	ARG	A	397	74.380	-9.284	39.196	1.00	15.59
2184	CB	ARG	A	397	74.185	-12.040	38.027	1.00	18.60
2185	CG	ARG	A	397	73.784	-13.316	37.287	1.00	19.84
2186	CD	ARG	A	397	72.553	-13.420	36.379	1.00	24.90
2187	NE	ARG	A	397	72.208	-14.621	35.612	1.00	22.76
2188	CZ	ARG	A	397	71.025	-14.402	35.008	1.00	23.41
2189	NH1	ARG	A	397	70.886	-13.392	34.144	1.00	19.94
2190	NH2	ARG	A	397	70.123	-15.367	35.053	1.00	23.58
2191	N	ALA	A	398	76.346	-9.296	38.010	1.00	16.37
2192	CA	ALA	A	398	77.067	-8.350	38.855	1.00	17.06
2193	C	ALA	A	398	78.247	-7.820	38.038	1.00	15.40
2194	O	ALA	A	398	78.597	-8.413	37.006	1.00	15.82
2195	CB	ALA	A	398	77.565	-9.054	40.119	1.00	16.67
2196	N	ILE	A	399	78.785	-6.669	38.345	1.00	15.06
2197	CA	ILE	A	399	79.836	-6.039	37.572	1.00	15.89
2198	C	ILE	A	399	80.901	-5.366	38.448	1.00	17.93
2199	O	ILE	A	399	80.735	-5.221	39.663	1.00	15.09
2200	CB	ILE	A	399	79.242	-4.896	36.717	1.00	15.87
2201	CG1	ILE	A	399	78.242	-4.078	37.530	1.00	16.12
2202	CG2	ILE	A	399	78.528	-5.438	35.467	1.00	18.19
2203	CD1	ILE	A	399	77.845	-2.740	36.874	1.00	16.62
2204	N	SER	A	400	81.929	-4.847	37.736	1.00	16.57
2205	CA	SER	A	400	82.921	-3.993	38.409	1.00	15.56

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2206	C	SER	A	400	82.236	-2.619	38.438	1.00	17.27
2207	O	SER	A	400	81.271	-2.466	37.653	1.00	16.46
2208	CB	SER	A	400	84.181	-3.946	37.561	1.00	15.65
2209	OG	SER	A	400	83.953	-3.310	36.304	1.00	15.40
2210	N	VAL	A	401	82.765	-1.616	39.082	1.00	15.63
2211	CA	VAL	A	401	82.217	-0.260	39.027	1.00	16.67
2212	C	VAL	A	401	82.096	0.223	37.617	1.00	18.39
2213	O	VAL	A	401	83.057	0.177	36.827	1.00	19.89
2214	CB	VAL	A	401	83.072	0.692	39.881	1.00	17.74
2215	CG1	VAL	A	401	82.552	2.095	39.678	1.00	16.22
2216	CG2	VAL	A	401	83.009	0.220	41.367	1.00	16.84
2217	N	ASN	A	402	80.936	0.785	37.203	1.00	19.45
2218	CA	ASN	A	402	80.780	1.251	35.824	1.00	19.83
2219	C	ASN	A	402	80.895	0.145	34.794	1.00	19.97
2220	O	ASN	A	402	81.048	0.448	33.599	1.00	19.00
2221	CB	ASN	A	402	81.846	2.355	35.598	1.00	19.30
2222	CG	ASN	A	402	81.421	3.707	36.135	1.00	19.90
2223	OD1	ASN	A	402	82.255	4.564	36.508	1.00	22.70
2224	ND2	ASN	A	402	80.134	3.976	36.206	1.00	13.99
2225	N	ALA	A	403	80.760	-1.136	35.122	1.00	19.56
2226	CA	ALA	A	403	80.744	-2.240	34.195	1.00	19.22
2227	C	ALA	A	403	81.897	-2.271	33.197	1.00	20.03
2228	O	ALA	A	403	81.731	-2.512	31.990	1.00	19.77
2229	CB	ALA	A	403	79.404	-2.200	33.423	1.00	19.35
2230	N	THR	A	404	83.131	-2.081	33.640	1.00	19.82
2231	CA	THR	A	404	84.301	-2.251	32.776	1.00	18.92
2232	C	THR	A	404	84.452	-3.747	32.583	1.00	19.28
2233	O	THR	A	404	85.132	-4.210	31.650	1.00	19.93
2234	CB	THR	A	404	85.587	-1.740	33.443	1.00	19.67
2235	OG1	THR	A	404	85.795	-2.458	34.677	1.00	17.98
2236	CG2	THR	A	404	85.515	-0.275	33.830	1.00	19.70
2237	N	ARG	A	405	83.995	-4.583	33.519	1.00	18.67
2238	CA	ARG	A	405	84.057	-6.024	33.509	1.00	16.48
2239	C	ARG	A	405	82.819	-6.658	34.168	1.00	17.16
2240	O	ARG	A	405	82.173	-5.960	34.970	1.00	16.14
2241	CB	ARG	A	405	85.261	-6.496	34.398	1.00	17.15
2242	CG	ARG	A	405	86.612	-5.917	33.939	1.00	17.89
2243	CD	ARG	A	405	87.772	-6.025	34.923	1.00	18.82
2244	NE	ARG	A	405	88.983	-5.382	34.421	1.00	18.77
2245	CZ	ARG	A	405	90.220	-5.421	34.908	1.00	19.96
2246	NH1	ARG	A	405	90.555	-6.060	36.027	1.00	17.06
2247	NH2	ARG	A	405	91.142	-4.729	34.232	1.00	19.62
2248	N	GLY	A	406	82.544	-7.922	33.884	1.00	15.61
2249	CA	GLY	A	406	81.431	-8.620	34.562	1.00	16.45
2250	C	GLY	A	406	82.102	-9.320	35.780	1.00	18.96
2251	O	GLY	A	406	83.334	-9.449	35.807	1.00	16.60
2252	N	MET	A	407	81.317	-9.686	36.773	1.00	18.47
2253	CA	MET	A	407	81.762	-10.295	38.010	1.00	18.88
2254	C	MET	A	407	81.015	-11.578	38.326	1.00	18.40
2255	O	MET	A	407	79.775	-11.615	38.240	1.00	17.72
2256	CB	MET	A	407	81.542	-9.323	39.182	1.00	18.65
2257	CG	MET	A	407	82.166	-9.673	40.526	1.00	16.86
2258	SD	MET	A	407	81.647	-8.523	41.829	1.00	16.73
2259	CE	MET	A	407	82.557	-9.127	43.234	1.00	19.44
2260	N	ILE	A	408	81.750	-12.645	38.616	1.00	16.52
2261	CA	ILE	A	408	81.201	-13.950	38.956	1.00	14.94
2262	C	ILE	A	408	80.888	-13.997	40.454	1.00	18.17
2263	O	ILE	A	408	81.786	-13.697	41.268	1.00	19.12
2264	CB	ILE	A	408	82.249	-15.018	38.606	1.00	15.45
2265	CG1	ILE	A	408	82.565	-15.005	37.081	1.00	15.33
2266	CG2	ILE	A	408	81.742	-16.389	39.050	1.00	16.59
2267	CD1	ILE	A	408	84.051	-15.308	36.771	1.00	17.24
2268	N	VAL	A	409	79.647	-14.260	40.875	1.00	16.48
2269	CA	VAL	A	409	79.309	-14.206	42.292	1.00	18.09
2270	C	VAL	A	409	78.466	-15.386	42.736	1.00	19.37
2271	O	VAL	A	409	77.906	-16.108	41.930	1.00	20.30
2272	CB	VAL	A	409	78.544	-12.920	42.668	1.00	17.54
2273	CG1	VAL	A	409	79.352	-11.657	42.436	1.00	14.93
2274	CG2	VAL	A	409	77.237	-12.727	41.871	1.00	18.02
2275	N	ASP	A	410	78.372	-15.587	44.041	1.00	21.46
2276	CA	ASP	A	410	77.548	-16.630	44.651	1.00	23.20
2277	C	ASP	A	410	76.213	-15.995	45.035	1.00	22.82
2278	O	ASP	A	410	76.182	-15.290	46.065	1.00	22.94
2279	CB	ASP	A	410	78.239	-17.131	45.946	1.00	23.65
2280	CG	ASP	A	410	77.474	-18.262	46.611	1.00	24.86
2281	OD1	ASP	A	410	76.311	-18.535	46.249	1.00	25.50
2282	OD2	ASP	A	410	78.060	-18.934	47.490	1.00	27.15
2283	N	LEU	A	411	75.146	-16.167	44.271	1.00	21.42
2284	CA	LEU	A	411	73.882	-15.508	44.506	1.00	21.38
2285	C	LEU	A	411	73.237	-15.851	45.845	1.00	22.44
2286	O	LEU	A	411	72.566	-14.989	46.436	1.00	19.95
2287	CB	LEU	A	411	72.876	-15.820	43.360	1.00	20.60
2288	CG	LEU	A	411	73.222	-15.156	42.010	1.00	20.02
2289	CD1	LEU	A	411	72.363	-15.723	40.902	1.00	16.46
2290	CD2	LEU	A	411	73.133	-13.644	42.152	1.00	19.54
2291	N	LYS	A	412	73.415	-17.079	46.331	1.00	21.58
2292	CA	LYS	A	412	72.795	-17.452	47.612	1.00	22.40
2293	C	LYS	A	412	73.254	-16.679	48.824	1.00	22.02
2294	O	LYS	A	412	72.506	-16.191	49.703	1.00	22.52
2295	CB	LYS	A	412	73.028	-18.966	47.842	1.00	26.92
2296	CG	LYS	A	412	72.311	-19.472	49.084	1.00	31.49
2297	CD	LYS	A	412	70.825	-19.669	48.788	1.00	33.84
2298	CE	LYS	A	412	70.110	-19.953	50.118	1.00	37.42
2299	NZ	LYS	A	412	70.382	-18.751	50.970	1.00	40.45
2300	N	ALA	A	413	74.517	-16.248	48.810	1.00	18.93
2301	CA	ALA	A	413	75.194	-15.455	49.803	1.00	20.77

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2302	C	ALA A 413	74.716	-14.003	49.860	1.00	20.66
2303	O	ALA A 413	74.909	-13.273	50.842	1.00	21.58
2304	CB	ALA A 413	76.696	-15.412	49.507	1.00	19.90
2305	N	THR A 414	74.083	-13.550	48.779	1.00	19.42
2306	CA	THR A 414	73.566	-12.207	48.706	1.00	20.42
2307	C	THR A 414	72.181	-12.039	49.330	1.00	22.20
2308	O	THR A 414	71.750	-10.883	49.514	1.00	20.49
2309	CB	THR A 414	73.489	-11.665	47.263	1.00	20.49
2310	OG1	THR A 414	72.430	-12.401	46.619	1.00	21.35
2311	CG2	THR A 414	74.770	-11.821	46.451	1.00	19.00
2312	N	ASP A 415	71.470	-13.097	49.627	1.00	21.64
2313	CA	ASP A 415	70.149	-13.115	50.208	1.00	21.34
2314	C	ASP A 415	70.129	-12.642	51.661	1.00	20.48
2315	O	ASP A 415	70.955	-13.100	52.457	1.00	21.23
2316	CB	ASP A 415	69.544	-14.522	50.278	1.00	21.16
2317	CG	ASP A 415	69.327	-15.177	48.937	1.00	23.55
2318	OD1	ASP A 415	69.131	-14.545	47.881	1.00	22.11
2319	OD2	ASP A 415	69.342	-16.414	48.905	1.00	24.37
2320	N	PRO A 416	69.298	-11.654	51.921	1.00	18.99
2321	CA	PRO A 416	69.131	-11.131	53.268	1.00	18.59
2322	C	PRO A 416	68.487	-12.203	54.143	1.00	19.83
2323	O	PRO A 416	67.848	-13.131	53.613	1.00	16.95
2324	CB	PRO A 416	68.177	-9.955	53.092	1.00	18.50
2325	CG	PRO A 416	67.383	-10.255	51.848	1.00	18.19
2326	CD	PRO A 416	68.355	-11.017	50.963	1.00	18.15
2327	N	ALA A 417	68.584	-12.001	55.459	1.00	19.41
2328	CA	ALA A 417	67.928	-12.898	56.410	1.00	18.88
2329	C	ALA A 417	66.416	-12.866	56.226	1.00	19.84
2330	O	ALA A 417	65.795	-11.828	55.964	1.00	19.83
2331	CB	ALA A 417	68.258	-12.437	57.822	1.00	18.37
2332	N	GLY A 418	65.790	-14.020	56.379	1.00	21.41
2333	CA	GLY A 418	64.368	-14.233	56.237	1.00	23.22
2334	C	GLY A 418	63.846	-14.337	54.810	1.00	23.60
2335	O	GLY A 418	62.643	-14.572	54.590	1.00	22.08
2336	N	TRP A 419	64.710	-14.183	53.807	1.00	23.46
2337	CA	TRP A 419	64.402	-14.234	52.396	1.00	23.20
2338	C	TRP A 419	63.606	-15.472	52.012	1.00	25.42
2339	O	TRP A 419	62.668	-15.373	51.199	1.00	24.03
2340	CB	TRP A 419	65.670	-14.233	51.530	1.00	22.84
2341	CG	TRP A 419	65.454	-13.984	50.043	1.00	22.68
2342	CD1	TRP A 419	65.788	-14.816	48.989	1.00	21.27
2343	CD2	TRP A 419	64.806	-12.860	49.459	1.00	20.14
2344	NE1	TRP A 419	65.454	-14.166	47.813	1.00	22.72
2345	CE2	TRP A 419	64.841	-12.969	48.060	1.00	21.05
2346	CE3	TRP A 419	64.233	-11.704	50.009	1.00	21.41
2347	CZ2	TRP A 419	64.305	-12.027	47.163	1.00	20.75
2348	CZ3	TRP A 419	63.711	-10.769	49.147	1.00	22.68
2349	CH2	TRP A 419	63.761	-10.889	47.753	1.00	21.75
2350	N	GLN A 420	63.929	-16.638	52.581	1.00	26.47
2351	CA	GLN A 420	63.179	-17.861	52.325	1.00	29.80
2352	C	GLN A 420	61.719	-17.770	52.728	1.00	28.92
2353	O	GLN A 420	60.919	-18.452	52.090	1.00	28.66
2354	CB	GLN A 420	63.849	-19.089	52.961	1.00	33.14
2355	CG	GLN A 420	64.919	-19.737	52.090	1.00	39.56
2356	CD	GLN A 420	64.607	-19.919	50.614	1.00	41.28
2357	OE1	GLN A 420	65.071	-19.074	49.835	1.00	43.54
2358	NE2	GLN A 420	63.849	-20.928	50.243	1.00	43.71
2359	N	GLY A 421	61.326	-16.936	53.690	1.00	29.02
2360	CA	GLY A 421	59.929	-16.790	54.080	1.00	27.43
2361	C	GLY A 421	59.223	-15.673	53.308	1.00	28.32
2362	O	GLY A 421	58.048	-15.418	53.556	1.00	24.66
2363	N	ASP A 422	59.878	-15.004	52.358	1.00	28.80
2364	CA	ASP A 422	59.295	-13.889	51.627	1.00	30.89
2365	C	ASP A 422	58.088	-14.200	50.738	1.00	36.19
2366	O	ASP A 422	58.230	-14.870	49.727	1.00	38.46
2367	CB	ASP A 422	60.420	-13.227	50.804	1.00	27.10
2368	CG	ASP A 422	59.951	-11.980	50.032	1.00	25.30
2369	OD1	ASP A 422	59.222	-11.152	50.594	1.00	23.55
2370	OD2	ASP A 422	60.287	-11.929	48.830	1.00	22.98
2371	N	HIS A 423	56.911	-13.629	51.020	1.00	40.93
2372	CA	HIS A 423	55.703	-13.849	50.233	1.00	47.21
2373	C	HIS A 423	55.313	-12.763	49.209	1.00	45.35
2374	O	HIS A 423	54.768	-11.681	49.406	1.00	47.07
2375	CB	HIS A 423	54.512	-14.100	51.176	1.00	51.41
2376	CG	HIS A 423	53.238	-14.617	50.601	1.00	56.21
2377	ND1	HIS A 423	52.275	-13.795	50.033	1.00	58.05
2378	CD2	HIS A 423	52.745	-15.896	50.562	1.00	57.47
2379	CE1	HIS A 423	51.265	-14.568	49.639	1.00	58.60
2380	NE2	HIS A 423	51.519	-15.838	49.939	1.00	58.38
2381	N	GLU A 424	55.414	-13.228	47.961	1.00	43.93
2382	CA	GLU A 424	54.955	-12.662	46.717	1.00	41.46
2383	C	GLU A 424	53.561	-12.097	47.029	1.00	35.89
2384	O	GLU A 424	52.765	-12.666	47.764	1.00	32.50
2385	CB	GLU A 424	54.860	-13.614	45.537	1.00	45.39
2386	CG	GLU A 424	53.602	-14.436	45.385	1.00	50.15
2387	CD	GLU A 424	53.588	-15.845	45.929	1.00	53.14
2388	OE1	GLU A 424	52.472	-16.435	45.889	1.00	55.07
2389	OE2	GLU A 424	54.628	-16.378	46.392	1.00	54.61
2390	N	GLN A 425	53.341	-10.927	46.478	1.00	31.51
2391	CA	GLN A 425	52.114	-10.187	46.730	1.00	30.43
2392	C	GLN A 425	51.336	-9.895	45.465	1.00	27.84
2393	O	GLN A 425	51.444	-8.806	44.889	1.00	25.73
2394	CB	GLN A 425	52.513	-8.862	47.412	1.00	28.91
2395	CG	GLN A 425	52.923	-9.100	48.863	1.00	31.80
2396	CD	GLN A 425	51.701	-9.408	49.711	1.00	34.90
2397	OE1	GLN A 425	51.857	-10.238	50.604	1.00	35.50

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2398	NE2	GLN	A	425	50.583	-8.779	49.384	1.00	34.92
2399	N	THR	A	426	50.650	-10.924	44.981	1.00	25.79
2400	CA	THR	A	426	49.878	-10.700	43.722	1.00	25.43
2401	C	THR	A	426	48.438	-11.054	44.030	1.00	24.91
2402	O	THR	A	426	48.194	-12.077	44.673	1.00	25.67
2403	CB	THR	A	426	50.462	-11.587	42.625	1.00	24.59
2404	OG1	THR	A	426	50.660	-12.926	43.104	1.00	26.94
2405	CG2	THR	A	426	51.843	-11.146	42.152	1.00	25.00
2406	N	PRO	A	427	47.481	-10.229	43.662	1.00	24.58
2407	CA	PRO	A	427	46.078	-10.493	43.995	1.00	22.44
2408	C	PRO	A	427	45.481	-11.448	42.987	1.00	19.97
2409	O	PRO	A	427	46.143	-11.846	42.015	1.00	18.98
2410	CB	PRO	A	427	45.449	-9.098	43.970	1.00	22.44
2411	CG	PRO	A	427	46.215	-8.410	42.886	1.00	23.34
2412	CD	PRO	A	427	47.643	-8.943	42.956	1.00	24.22
2413	N	ALA	A	428	44.221	-11.818	43.186	1.00	18.32
2414	CA	ALA	A	428	43.524	-12.705	42.287	1.00	18.67
2415	C	ALA	A	428	43.302	-12.115	40.901	1.00	18.67
2416	O	ALA	A	428	43.391	-12.950	39.990	1.00	18.53
2417	CB	ALA	A	428	42.176	-13.179	42.853	1.00	19.42
2418	N	ASN	A	429	43.248	-10.788	40.730	1.00	16.60
2419	CA	ASN	A	429	43.080	-10.263	39.358	1.00	15.96
2420	C	ASN	A	429	43.673	-8.877	39.366	1.00	16.94
2421	O	ASN	A	429	43.676	-8.221	40.413	1.00	17.66
2422	CB	ASN	A	429	41.572	-10.199	39.015	1.00	15.37
2423	CG	ASN	A	429	41.218	-9.874	37.587	1.00	14.52
2424	OD1	ASN	A	429	40.864	-10.725	36.749	1.00	17.02
2425	ND2	ASN	A	429	41.224	-8.619	37.164	1.00	12.11
2426	N	PRO	A	430	44.223	-8.379	38.259	1.00	17.36
2427	CA	PRO	A	430	44.798	-7.059	38.201	1.00	17.36
2428	C	PRO	A	430	43.884	-5.954	38.671	1.00	16.98
2429	O	PRO	A	430	44.439	-4.967	39.171	1.00	15.58
2430	CB	PRO	A	430	45.274	-6.889	36.756	1.00	17.72
2431	CG	PRO	A	430	45.459	-8.315	36.305	1.00	17.97
2432	CD	PRO	A	430	44.377	-9.110	36.977	1.00	16.18
2433	N	VAL	A	431	42.554	-5.999	38.575	1.00	16.77
2434	CA	VAL	A	431	41.696	-4.882	39.029	1.00	14.93
2435	C	VAL	A	431	41.724	-4.718	40.549	1.00	16.96
2436	O	VAL	A	431	41.207	-3.711	41.066	1.00	14.24
2437	CB	VAL	A	431	40.236	-5.000	38.552	1.00	14.61
2438	CG1	VAL	A	431	40.141	-5.164	37.018	1.00	11.37
2439	CG2	VAL	A	431	39.470	-6.174	39.204	1.00	9.63
2440	N	ASP	A	432	42.285	-5.672	41.303	1.00	15.55
2441	CA	ASP	A	432	42.506	-5.572	42.728	1.00	16.36
2442	C	ASP	A	432	43.735	-4.744	43.102	1.00	16.54
2443	O	ASP	A	432	43.956	-4.499	44.305	1.00	15.51
2444	CB	ASP	A	432	42.669	-6.988	43.365	1.00	14.88
2445	CG	ASP	A	432	41.447	-7.835	43.087	1.00	15.34
2446	OD1	ASP	A	432	40.318	-7.267	43.043	1.00	16.21
2447	OD2	ASP	A	432	41.488	-9.064	42.873	1.00	14.61
2448	N	GLU	A	433	44.537	-4.259	42.145	1.00	15.94
2449	CA	GLU	A	433	45.689	-3.429	42.512	1.00	16.94
2450	C	GLU	A	433	45.343	-1.946	42.441	1.00	16.06
2451	O	GLU	A	433	44.479	-1.513	41.664	1.00	16.07
2452	CB	GLU	A	433	46.942	-3.630	41.625	1.00	15.85
2453	CG	GLU	A	433	47.546	-5.015	41.739	1.00	16.52
2454	CD	GLU	A	433	48.933	-5.312	41.195	1.00	16.36
2455	OE1	GLU	A	433	49.492	-4.536	40.379	1.00	11.53
2456	OE2	GLU	A	433	49.449	-6.397	41.635	1.00	14.91
2457	N	VAL	A	434	46.021	-1.168	43.262	1.00	15.28
2458	CA	VAL	A	434	46.036	0.299	43.193	1.00	14.14
2459	C	VAL	A	434	47.553	0.628	43.106	1.00	15.28
2460	O	VAL	A	434	48.292	0.509	44.136	1.00	13.41
2461	CB	VAL	A	434	45.360	0.930	44.419	1.00	14.74
2462	CG1	VAL	A	434	45.241	2.440	44.130	1.00	14.68
2463	CG2	VAL	A	434	43.954	0.334	44.672	1.00	13.12
2464	N	ILE	A	435	48.014	1.058	41.947	1.00	14.64
2465	CA	ILE	A	435	49.459	1.202	41.665	1.00	13.40
2466	C	ILE	A	435	49.966	2.607	41.870	1.00	15.38
2467	O	ILE	A	435	49.312	3.525	41.385	1.00	17.74
2468	CB	ILE	A	435	49.775	0.758	40.228	1.00	14.42
2469	CG1	ILE	A	435	49.243	-0.693	40.023	1.00	14.98
2470	CG2	ILE	A	435	51.253	0.888	39.874	1.00	12.09
2471	CD1	ILE	A	435	49.227	-1.169	38.568	1.00	13.44
2472	N	TYR	A	436	51.082	2.759	42.563	1.00	13.59
2473	CA	TYR	A	436	51.698	4.037	42.855	1.00	15.25
2474	C	TYR	A	436	53.109	4.093	42.264	1.00	15.01
2475	O	TYR	A	436	53.988	3.279	42.617	1.00	14.02
2476	CB	TYR	A	436	51.711	4.156	44.367	1.00	15.52
2477	CG	TYR	A	436	52.196	5.355	45.116	1.00	16.16
2478	CD1	TYR	A	436	51.289	6.303	45.576	1.00	15.41
2479	CD2	TYR	A	436	53.549	5.498	45.460	1.00	15.75
2480	CE1	TYR	A	436	51.717	7.384	46.327	1.00	16.02
2481	CE2	TYR	A	436	53.987	6.584	46.218	1.00	15.63
2482	CZ	TYR	A	436	53.058	7.496	46.674	1.00	15.39
2483	OH	TYR	A	436	53.434	8.562	47.464	1.00	16.13
2484	N	GLU	A	437	53.329	4.992	41.304	1.00	15.46
2485	CA	GLU	A	437	54.622	5.123	40.620	1.00	15.46
2486	C	GLU	A	437	55.651	5.927	41.411	1.00	16.03
2487	O	GLU	A	437	55.329	7.076	41.747	1.00	17.07
2488	CB	GLU	A	437	54.458	5.834	39.263	1.00	15.08
2489	CG	GLU	A	437	55.716	5.978	38.411	1.00	14.65
2490	CD	GLU	A	437	55.493	6.596	37.048	1.00	14.65
2491	OE1	GLU	A	437	54.648	7.489	36.869	1.00	15.22
2492	OE2	GLU	A	437	56.087	6.145	36.035	1.00	16.08
2493	N	ALA	A	438	56.882	5.394	41.543	1.00	13.82

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2494	CA	ALA	A	438	57.878	6.186	42.253	1.00	13.55
2495	C	ALA	A	438	59.312	5.910	41.823	1.00	14.91
2496	O	ALA	A	438	59.721	4.775	41.558	1.00	13.87
2497	CB	ALA	A	438	57.660	5.898	43.765	1.00	13.69
2498	N	HIS	A	439	60.142	6.969	41.828	1.00	16.29
2499	CA	HIS	A	439	61.572	6.838	41.501	1.00	16.19
2500	C	HIS	A	439	62.351	6.603	42.805	1.00	16.70
2501	O	HIS	A	439	62.025	7.212	43.813	1.00	14.31
2502	CB	HIS	A	439	62.043	8.086	40.776	1.00	16.30
2503	CG	HIS	A	439	63.440	8.147	40.223	1.00	16.75
2504	ND1	HIS	A	439	64.518	8.470	41.049	1.00	15.99
2505	CD2	HIS	A	439	63.943	7.963	38.965	1.00	14.58
2506	CE1	HIS	A	439	65.624	8.516	40.288	1.00	17.06
2507	NE2	HIS	A	439	65.302	8.221	39.029	1.00	16.41
2508	N	VAL	A	440	63.328	5.687	42.858	1.00	15.20
2509	CA	VAL	A	440	64.031	5.389	44.106	1.00	15.25
2510	C	VAL	A	440	64.653	6.618	44.780	1.00	16.03
2511	O	VAL	A	440	64.516	6.773	45.999	1.00	16.04
2512	CB	VAL	A	440	65.116	4.317	43.867	1.00	15.02
2513	CG1	VAL	A	440	65.972	4.169	45.128	1.00	16.66
2514	CG2	VAL	A	440	64.459	2.977	43.508	1.00	15.14
2515	N	ARG	A	441	65.342	7.469	44.034	1.00	16.63
2516	CA	ARG	A	441	65.925	8.698	44.541	1.00	17.10
2517	C	ARG	A	441	64.899	9.740	45.000	1.00	17.55
2518	O	ARG	A	441	65.010	10.221	46.170	1.00	17.74
2519	CB	ARG	A	441	66.896	9.304	43.501	1.00	14.61
2520	CG	ARG	A	441	67.704	10.461	44.088	1.00	16.94
2521	CD	ARG	A	441	68.732	11.060	43.137	1.00	18.60
2522	NE	ARG	A	441	69.386	12.271	43.671	1.00	16.23
2523	CZ	ARG	A	441	70.470	12.234	44.458	1.00	17.59
2524	NH1	ARG	A	441	71.094	11.121	44.855	1.00	17.67
2525	NH2	ARG	A	441	71.002	13.363	44.893	1.00	17.22
2526	N	ASP	A	442	63.897	10.087	44.191	1.00	16.68
2527	CA	ASP	A	442	62.882	11.067	44.550	1.00	17.07
2528	C	ASP	A	442	62.150	10.781	45.865	1.00	15.50
2529	O	ASP	A	442	61.789	11.686	46.627	1.00	14.92
2530	CB	ASP	A	442	61.705	11.140	43.534	1.00	16.09
2531	CG	ASP	A	442	62.092	11.481	42.103	1.00	18.27
2532	OD1	ASP	A	442	61.161	11.472	41.265	1.00	16.61
2533	OD2	ASP	A	442	63.293	11.722	41.820	1.00	16.36
2534	N	PHE	A	443	61.865	9.519	46.113	1.00	14.50
2535	CA	PHE	A	443	61.090	9.094	47.277	1.00	14.57
2536	C	PHE	A	443	61.629	9.580	48.615	1.00	16.96
2537	O	PHE	A	443	60.820	9.958	49.474	1.00	15.43
2538	CB	PHE	A	443	61.104	7.553	47.333	1.00	15.23
2539	CG	PHE	A	443	60.077	7.005	48.292	1.00	16.07
2540	CD1	PHE	A	443	60.475	6.290	49.410	1.00	17.87
2541	CD2	PHE	A	443	58.722	7.225	48.081	1.00	17.50
2542	CE1	PHE	A	443	59.546	5.788	50.302	1.00	19.15
2543	CE2	PHE	A	443	57.797	6.682	48.961	1.00	19.87
2544	CZ	PHE	A	443	58.202	5.978	50.077	1.00	19.27
2545	N	SER	A	444	62.941	9.578	48.844	1.00	14.65
2546	CA	SER	A	444	63.491	10.014	50.121	1.00	16.85
2547	C	SER	A	444	64.692	10.959	50.081	1.00	17.60
2548	O	SER	A	444	65.223	11.288	51.168	1.00	17.78
2549	CB	SER	A	444	63.933	8.772	50.891	1.00	17.91
2550	OG	SER	A	444	64.813	8.072	50.004	1.00	18.93
2551	N	ILE	A	445	65.083	11.532	48.944	1.00	16.65
2552	CA	ILE	A	445	66.272	12.363	48.864	1.00	17.86
2553	C	ILE	A	445	66.133	13.664	49.641	1.00	19.05
2554	O	ILE	A	445	67.136	14.236	50.089	1.00	19.84
2555	CB	ILE	A	445	66.725	12.704	47.422	1.00	18.82
2556	CG1	ILE	A	445	68.114	13.345	47.373	1.00	19.76
2557	CG2	ILE	A	445	65.717	13.625	46.737	1.00	16.03
2558	CD1	ILE	A	445	69.261	12.451	47.830	1.00	17.68
2559	N	ASP	A	446	64.944	14.247	49.757	1.00	17.88
2560	CA	ASP	A	446	64.795	15.549	50.429	1.00	19.31
2561	C	ASP	A	446	65.343	15.527	51.856	1.00	18.39
2562	O	ASP	A	446	65.028	14.618	52.664	1.00	14.79
2563	CB	ASP	A	446	63.319	15.965	50.406	1.00	17.77
2564	CG	ASP	A	446	62.997	17.404	50.598	1.00	19.68
2565	OD1	ASP	A	446	62.211	18.007	49.823	1.00	20.47
2566	OD2	ASP	A	446	63.527	18.071	51.516	1.00	17.16
2567	N	ALA	A	447	65.955	16.640	52.293	1.00	19.59
2568	CA	ALA	A	447	66.372	16.734	53.696	1.00	20.17
2569	C	ALA	A	447	65.212	16.578	54.680	1.00	21.62
2570	O	ALA	A	447	65.444	16.179	55.845	1.00	20.80
2571	CB	ALA	A	447	67.086	18.077	53.958	1.00	22.60
2572	N	ASN	A	448	63.958	16.873	54.328	1.00	20.17
2573	CA	ASN	A	448	62.852	16.752	55.303	1.00	19.49
2574	C	ASN	A	448	62.130	15.408	55.274	1.00	20.38
2575	O	ASN	A	448	61.062	15.275	55.906	1.00	18.16
2576	CB	ASN	A	448	61.835	17.863	54.959	1.00	18.25
2577	CG	ASN	A	448	61.103	17.701	53.619	1.00	19.72
2578	OD1	ASN	A	448	61.019	16.634	52.997	1.00	19.01
2579	ND2	ASN	A	448	60.625	18.786	53.028	1.00	18.34
2580	N	SER	A	449	62.630	14.404	54.537	1.00	19.41
2581	CA	SER	A	449	61.917	13.131	54.370	1.00	20.28
2582	C	SER	A	449	61.780	12.255	55.599	1.00	20.00
2583	O	SER	A	449	60.950	11.332	55.677	1.00	20.48
2584	CB	SER	A	449	62.563	12.336	53.203	1.00	18.80
2585	OG	SER	A	449	63.731	11.616	53.593	1.00	16.39
2586	N	GLY	A	450	62.709	12.410	56.516	1.00	19.28
2587	CA	GLY	A	450	62.812	11.662	57.762	1.00	18.69
2588	C	GLY	A	450	63.495	10.312	57.606	1.00	19.34
2589	O	GLY	A	450	63.580	9.532	58.586	1.00	19.10

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2590	N	MET	A	451	63.897	9.939	56.412	1.00	17.66
2591	CA	MET	A	451	64.550	8.650	56.169	1.00	19.49
2592	C	MET	A	451	66.056	8.859	56.152	1.00	21.41
2593	O	MET	A	451	66.534	9.886	55.659	1.00	21.59
2594	CB	MET	A	451	64.044	8.109	54.818	1.00	18.54
2595	CG	MET	A	451	62.704	7.387	54.938	1.00	18.74
2596	SD	MET	A	451	61.951	7.071	53.330	1.00	15.90
2597	CE	MET	A	451	61.313	8.726	52.990	1.00	16.43
2598	N	LYS	A	452	66.849	7.964	56.728	1.00	24.96
2599	CA	LYS	A	452	68.292	8.105	56.755	1.00	25.67
2600	C	LYS	A	452	69.007	7.729	55.462	1.00	24.98
2601	O	LYS	A	452	69.976	8.421	55.111	1.00	22.58
2602	CB	LYS	A	452	68.865	7.134	57.821	1.00	29.87
2603	CG	LYS	A	452	68.343	7.423	59.227	1.00	34.10
2604	CD	LYS	A	452	69.048	6.450	60.162	1.00	38.10
2605	CE	LYS	A	452	68.830	6.729	61.640	1.00	40.92
2606	NZ	LYS	A	452	69.743	5.855	62.443	1.00	43.49
2607	N	ASN	A	453	68.621	6.628	54.808	1.00	22.30
2608	CA	ASN	A	453	69.323	6.230	53.583	1.00	22.25
2609	C	ASN	A	453	68.792	6.986	52.372	1.00	22.88
2610	O	ASN	A	453	68.213	6.412	51.448	1.00	20.10
2611	CB	ASN	A	453	69.185	4.732	53.390	1.00	22.17
2612	CG	ASN	A	453	69.885	3.894	54.438	1.00	22.47
2613	OD1	ASN	A	453	69.207	3.368	55.345	1.00	26.98
2614	ND2	ASN	A	453	71.168	3.715	54.360	1.00	18.00
2615	N	LYS	A	454	69.120	8.272	52.262	1.00	22.54
2616	CA	LYS	A	454	68.515	9.200	51.323	1.00	21.14
2617	C	LYS	A	454	68.895	8.936	49.881	1.00	20.78
2618	O	LYS	A	454	70.071	8.790	49.545	1.00	22.89
2619	CB	LYS	A	454	68.872	10.638	51.774	1.00	21.38
2620	CG	LYS	A	454	68.057	11.105	53.013	1.00	23.20
2621	CD	LYS	A	454	68.334	12.597	53.277	1.00	23.57
2622	CE	LYS	A	454	67.796	12.998	54.648	1.00	25.95
2623	NZ	LYS	A	454	66.341	12.839	54.758	1.00	26.08
2624	N	GLY	A	455	67.909	8.715	49.012	1.00	19.05
2625	CA	GLY	A	455	68.086	8.463	47.590	1.00	17.30
2626	C	GLY	A	455	68.350	7.013	47.242	1.00	17.20
2627	O	GLY	A	455	68.723	6.665	46.111	1.00	17.53
2628	N	LYS	A	456	68.270	6.123	48.226	1.00	15.28
2629	CA	LYS	A	456	68.659	4.734	48.032	1.00	16.32
2630	C	LYS	A	456	67.611	3.650	48.265	1.00	15.37
2631	O	LYS	A	456	66.603	3.951	48.904	1.00	15.63
2632	CB	LYS	A	456	69.787	4.424	49.040	1.00	18.28
2633	CG	LYS	A	456	70.918	5.434	49.114	1.00	18.06
2634	CD	LYS	A	456	72.081	4.992	48.231	1.00	19.93
2635	CE	LYS	A	456	73.093	6.121	48.121	1.00	20.50
2636	NZ	LYS	A	456	74.035	5.934	46.985	1.00	18.68
2637	N	TYR	A	457	67.870	2.454	47.758	1.00	14.15
2638	CA	TYR	A	457	66.986	1.341	47.981	1.00	13.53
2639	C	TYR	A	457	66.678	1.189	49.489	1.00	18.21
2640	O	TYR	A	457	65.487	1.011	49.788	1.00	13.29
2641	CB	TYR	A	457	67.490	-0.024	47.538	1.00	13.55
2642	CG	TYR	A	457	67.956	-0.142	46.075	1.00	14.83
2643	CD1	TYR	A	457	69.241	-0.546	45.761	1.00	15.53
2644	CD2	TYR	A	457	67.107	0.110	45.014	1.00	15.14
2645	CE1	TYR	A	457	69.663	-0.645	44.409	1.00	15.97
2646	CE2	TYR	A	457	67.460	0.018	43.665	1.00	15.67
2647	CZ	TYR	A	457	68.762	-0.369	43.408	1.00	16.86
2648	OH	TYR	A	457	69.165	-0.482	42.066	1.00	18.18
2649	N	LEU	A	458	67.603	1.255	50.450	1.00	17.70
2650	CA	LEU	A	458	67.335	0.919	51.869	1.00	18.01
2651	C	LEU	A	458	66.370	1.882	52.549	1.00	15.81
2652	O	LEU	A	458	65.802	1.650	53.669	1.00	14.97
2653	CB	LEU	A	458	68.678	0.861	52.699	1.00	17.40
2654	CG	LEU	A	458	69.584	-0.333	52.378	1.00	17.94
2655	CD1	LEU	A	458	70.830	-0.312	53.282	1.00	20.17
2656	CD2	LEU	A	458	68.866	-1.692	52.511	1.00	17.60
2657	N	ALA	A	459	66.132	3.071	51.984	1.00	15.65
2658	CA	ALA	A	459	65.167	4.005	52.608	1.00	16.80
2659	C	ALA	A	459	63.772	3.381	52.772	1.00	18.08
2660	O	ALA	A	459	63.016	3.656	53.718	1.00	15.52
2661	CB	ALA	A	459	65.103	5.260	51.750	1.00	14.58
2662	N	PHE	A	460	63.361	2.510	51.838	1.00	16.60
2663	CA	PHE	A	460	62.117	1.786	51.868	1.00	18.35
2664	C	PHE	A	460	62.017	0.683	52.942	1.00	19.16
2665	O	PHE	A	460	60.944	0.074	53.052	1.00	16.71
2666	CB	PHE	A	460	61.813	1.132	50.518	1.00	19.39
2667	CG	PHE	A	460	61.495	2.064	49.369	1.00	19.42
2668	CD1	PHE	A	460	60.199	2.051	48.869	1.00	22.23
2669	CD2	PHE	A	460	62.477	2.748	48.693	1.00	19.19
2670	CE1	PHE	A	460	59.853	2.859	47.787	1.00	20.33
2671	CE2	PHE	A	460	62.162	3.544	47.607	1.00	20.31
2672	CZ	PHE	A	460	60.847	3.590	47.141	1.00	20.55
2673	N	THR	A	461	63.086	0.410	53.727	1.00	17.62
2674	CA	THR	A	461	63.041	-0.515	54.824	1.00	17.58
2675	C	THR	A	461	62.842	0.254	56.179	1.00	17.98
2676	O	THR	A	461	62.824	-0.422	57.195	1.00	17.01
2677	CB	THR	A	461	64.340	-1.338	55.019	1.00	17.81
2678	OG1	THR	A	461	65.418	-0.430	55.344	1.00	16.28
2679	CG2	THR	A	461	64.706	-2.058	53.713	1.00	18.33
2680	N	GLU	A	462	62.820	1.569	56.197	1.00	17.91
2681	CA	GLU	A	462	62.881	2.254	57.509	1.00	18.73
2682	C	GLU	A	462	61.452	2.526	58.028	1.00	20.80
2683	O	GLU	A	462	60.651	3.247	57.389	1.00	17.17
2684	CB	GLU	A	462	63.597	3.584	57.237	1.00	19.94
2685	CG	GLU	A	462	65.032	3.372	56.651	1.00	20.13

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2686	CD	GLU	A	462	65.759	4.695	56.580	1.00	21.29
2687	OE1	GLU	A	462	65.461	5.602	57.401	1.00	22.06
2688	OE2	GLU	A	462	66.629	4.885	55.702	1.00	20.07
2689	N	HIS	A	463	61.096	1.977	59.194	1.00	20.54
2690	CA	HIS	A	463	59.806	2.170	59.831	1.00	22.30
2691	C	HIS	A	463	59.778	3.350	60.778	1.00	22.71
2692	O	HIS	A	463	60.819	3.655	61.359	1.00	23.44
2693	CB	HIS	A	463	59.476	0.918	60.666	1.00	24.53
2694	CG	HIS	A	463	59.062	-0.209	59.775	1.00	26.84
2695	ND1	HIS	A	463	59.954	-1.062	59.187	1.00	29.88
2696	CD2	HIS	A	463	57.841	-0.611	59.362	1.00	28.11
2697	CE1	HIS	A	463	59.315	-1.954	58.450	1.00	29.51
2698	NE2	HIS	A	463	58.029	-1.696	58.538	1.00	30.87
2699	N	GLY	A	464	58.637	3.962	61.066	1.00	23.85
2700	CA	GLY	A	464	58.547	5.049	62.031	1.00	22.89
2701	C	GLY	A	464	59.042	6.398	61.558	1.00	23.91
2702	O	GLY	A	464	59.256	7.293	62.406	1.00	21.28
2703	N	THR	A	465	59.227	6.617	60.250	1.00	21.74
2704	CA	THR	A	465	59.815	7.888	59.806	1.00	21.41
2705	C	THR	A	465	58.782	8.990	59.735	1.00	21.03
2706	O	THR	A	465	57.602	8.744	59.460	1.00	23.25
2707	CB	THR	A	465	60.563	7.738	58.467	1.00	22.09
2708	OG1	THR	A	465	59.630	7.327	57.447	1.00	20.70
2709	CG2	THR	A	465	61.643	6.667	58.699	1.00	21.72
2710	N	LYS	A	466	59.185	10.189	60.070	1.00	19.33
2711	CA	LYS	A	466	58.343	11.334	60.285	1.00	21.71
2712	C	LYS	A	466	58.905	12.549	59.557	1.00	21.36
2713	O	LYS	A	466	60.121	12.630	59.456	1.00	22.34
2714	CB	LYS	A	466	58.316	11.761	61.775	1.00	22.16
2715	CG	LYS	A	466	57.913	10.655	62.722	1.00	25.69
2716	CD	LYS	A	466	56.511	10.112	62.448	1.00	27.19
2717	CE	LYS	A	466	56.168	9.053	63.502	1.00	29.76
2718	NZ	LYS	A	466	54.932	8.298	63.127	1.00	29.77
2719	N	GLY	A	467	58.029	13.410	59.087	1.00	20.73
2720	CA	GLY	A	467	58.437	14.611	58.385	1.00	22.16
2721	C	GLY	A	467	57.855	15.833	59.110	1.00	23.57
2722	O	GLY	A	467	57.559	15.770	60.300	1.00	21.29
2723	N	PRO	A	468	57.742	16.944	58.387	1.00	24.04
2724	CA	PRO	A	468	57.264	18.188	58.952	1.00	24.86
2725	C	PRO	A	468	55.921	18.023	59.638	1.00	26.71
2726	O	PRO	A	468	55.032	17.290	59.223	1.00	24.09
2727	CB	PRO	A	468	57.252	19.135	57.761	1.00	24.51
2728	CG	PRO	A	468	58.442	18.647	56.967	1.00	24.08
2729	CD	PRO	A	468	58.260	17.127	57.004	1.00	23.34
2730	N	ASP	A	469	55.809	18.622	60.845	1.00	28.85
2731	CA	ASP	A	469	54.568	18.580	61.605	1.00	31.00
2732	C	ASP	A	469	54.190	17.167	62.012	1.00	29.54
2733	O	ASP	A	469	53.005	16.831	62.142	1.00	25.09
2734	CB	ASP	A	469	53.429	19.166	60.762	1.00	35.81
2735	CG	ASP	A	469	53.461	20.687	60.704	1.00	41.18
2736	OD1	ASP	A	469	54.229	21.361	61.442	1.00	42.60
2737	OD2	ASP	A	469	52.675	21.251	59.899	1.00	42.71
2738	N	HIS	A	470	55.216	16.314	62.194	1.00	27.09
2739	CA	HIS	A	470	54.991	14.943	62.567	1.00	29.90
2740	C	HIS	A	470	54.158	14.124	61.571	1.00	27.51
2741	O	HIS	A	470	53.713	13.036	61.986	1.00	25.40
2742	CB	HIS	A	470	54.351	14.933	63.968	1.00	35.53
2743	CG	HIS	A	470	54.966	13.762	64.690	1.00	41.88
2744	ND1	HIS	A	470	54.293	12.781	65.341	1.00	44.60
2745	CD2	HIS	A	470	56.338	13.553	64.868	1.00	44.13
2746	CE1	HIS	A	470	55.239	11.999	65.896	1.00	45.27
2747	NE2	HIS	A	470	56.472	12.438	65.630	1.00	45.71
2748	N	VAL	A	471	54.101	14.443	60.279	1.00	24.01
2749	CA	VAL	A	471	53.376	13.539	59.370	1.00	22.37
2750	C	VAL	A	471	54.211	12.254	59.214	1.00	21.98
2751	O	VAL	A	471	55.442	12.318	59.299	1.00	20.13
2752	CB	VAL	A	471	53.104	14.132	57.982	1.00	21.65
2753	CG1	VAL	A	471	52.190	15.365	58.015	1.00	19.93
2754	CG2	VAL	A	471	54.419	14.466	57.278	1.00	20.15
2755	N	LYS	A	472	53.542	11.139	58.935	1.00	19.69
2756	CA	LYS	A	472	54.244	9.876	58.649	1.00	18.37
2757	C	LYS	A	472	54.846	9.942	57.237	1.00	17.74
2758	O	LYS	A	472	54.211	10.506	56.321	1.00	17.56
2759	CB	LYS	A	472	53.212	8.750	58.700	1.00	21.16
2760	CG	LYS	A	472	52.495	8.535	60.043	1.00	20.15
2761	CD	LYS	A	472	51.529	7.341	59.924	1.00	21.24
2762	CE	LYS	A	472	51.192	6.810	61.317	1.00	25.17
2763	NZ	LYS	A	472	50.187	5.690	61.273	1.00	26.92
2764	N	THR	A	473	56.073	9.506	56.991	1.00	16.26
2765	CA	THR	A	473	56.650	9.508	55.639	1.00	17.04
2766	C	THR	A	473	57.096	8.108	55.226	1.00	16.39
2767	O	THR	A	473	56.881	7.201	56.041	1.00	14.08
2768	CB	THR	A	473	57.916	10.402	55.585	1.00	17.28
2769	OG1	THR	A	473	58.862	9.885	56.543	1.00	17.62
2770	CG2	THR	A	473	57.590	11.827	56.000	1.00	15.72
2771	N	GLY	A	474	57.706	7.921	54.044	1.00	15.36
2772	CA	GLY	A	474	58.229	6.588	53.720	1.00	15.08
2773	C	GLY	A	474	57.174	5.503	53.681	1.00	17.27
2774	O	GLY	A	474	55.985	5.776	53.434	1.00	15.09
2775	N	ILE	A	475	57.568	4.262	53.897	1.00	18.67
2776	CA	ILE	A	475	56.630	3.138	53.914	1.00	20.49
2777	C	ILE	A	475	55.474	3.256	54.907	1.00	19.29
2778	O	ILE	A	475	54.377	2.749	54.563	1.00	18.42
2779	CB	ILE	A	475	57.414	1.826	54.113	1.00	22.81
2780	CG1	ILE	A	475	56.478	0.702	53.724	1.00	24.37
2781	CG2	ILE	A	475	57.885	1.646	55.592	1.00	21.69

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2782	CD1	ILE	A	475	57.108	-0.682	53.618	1.00	28.52
2783	N	ASP	A	476	55.616	3.969	56.026	1.00	17.17
2784	CA	ASP	A	476	54.413	4.168	56.891	1.00	17.44
2785	C	ASP	A	476	53.387	5.060	56.185	1.00	16.48
2786	O	ASP	A	476	52.197	4.895	56.429	1.00	15.25
2787	CB	ASP	A	476	54.756	4.796	58.234	1.00	16.38
2788	CG	ASP	A	476	55.480	3.874	59.211	1.00	18.13
2789	OD1	ASP	A	476	55.930	4.354	60.259	1.00	17.91
2790	OD2	ASP	A	476	55.639	2.680	58.915	1.00	16.55
2791	N	SER	A	477	53.786	6.034	55.354	1.00	16.25
2792	CA	SER	A	477	52.848	6.880	54.629	1.00	16.55
2793	C	SER	A	477	52.108	6.065	53.549	1.00	18.34
2794	O	SER	A	477	50.912	6.237	53.283	1.00	19.12
2795	CB	SER	A	477	53.532	8.086	53.987	1.00	15.71
2796	OG	SER	A	477	52.610	8.857	53.192	1.00	17.49
2797	N	LEU	A	478	52.825	5.184	52.841	1.00	18.20
2798	CA	LEU	A	478	52.237	4.299	51.853	1.00	17.44
2799	C	LEU	A	478	51.154	3.403	52.475	1.00	19.05
2800	O	LEU	A	478	50.062	3.242	51.912	1.00	16.99
2801	CB	LEU	A	478	53.296	3.419	51.195	1.00	17.36
2802	CG	LEU	A	478	54.412	4.051	50.367	1.00	18.83
2803	CD1	LEU	A	478	55.262	2.927	49.763	1.00	20.70
2804	CD2	LEU	A	478	53.898	5.003	49.304	1.00	17.67
2805	N	LYS	A	479	51.418	2.843	53.647	1.00	20.29
2806	CA	LYS	A	479	50.448	2.085	54.413	1.00	23.91
2807	C	LYS	A	479	49.209	2.910	54.724	1.00	22.75
2808	O	LYS	A	479	48.056	2.535	54.473	1.00	23.72
2809	CB	LYS	A	479	51.049	1.642	55.759	1.00	27.33
2810	CG	LYS	A	479	50.226	0.539	56.358	1.00	32.76
2811	CD	LYS	A	479	50.636	-0.179	57.602	1.00	37.03
2812	CE	LYS	A	479	52.051	-0.291	58.088	1.00	40.23
2813	NZ	LYS	A	479	52.935	-1.004	57.114	1.00	42.37
2814	N	GLU	A	480	49.388	4.126	55.242	1.00	21.40
2815	CA	GLU	A	480	48.229	4.920	55.588	1.00	22.52
2816	C	GLU	A	480	47.449	5.378	54.364	1.00	19.27
2817	O	GLU	A	480	46.229	5.531	54.458	1.00	16.95
2818	CB	GLU	A	480	48.490	6.066	56.547	1.00	25.40
2819	CG	GLU	A	480	49.133	7.273	55.983	1.00	28.08
2820	CD	GLU	A	480	49.042	8.444	56.945	1.00	30.33
2821	OE1	GLU	A	480	48.009	8.573	57.618	1.00	33.89
2822	OE2	GLU	A	480	49.967	9.261	57.025	1.00	26.83
2823	N	LEU	A	481	48.091	5.482	53.220	1.00	19.95
2824	CA	LEU	A	481	47.406	5.891	51.984	1.00	16.96
2825	C	LEU	A	481	46.484	4.792	51.463	1.00	17.11
2826	O	LEU	A	481	45.404	5.121	50.925	1.00	15.46
2827	CB	LEU	A	481	48.502	6.240	50.976	1.00	17.20
2828	CG	LEU	A	481	48.070	6.823	49.640	1.00	17.62
2829	CD1	LEU	A	481	47.221	8.098	49.831	1.00	16.14
2830	CD2	LEU	A	481	49.273	7.277	48.811	1.00	14.35
2831	N	GLY	A	482	46.845	3.526	51.664	1.00	15.48
2832	CA	GLY	A	482	46.042	2.419	51.161	1.00	15.68
2833	C	GLY	A	482	46.507	1.767	49.851	1.00	16.09
2834	O	GLY	A	482	45.908	0.771	49.461	1.00	14.56
2835	N	ILE	A	483	47.483	2.333	49.124	1.00	15.13
2836	CA	ILE	A	483	47.942	1.737	47.849	1.00	15.05
2837	C	ILE	A	483	48.385	0.301	48.077	1.00	15.90
2838	O	ILE	A	483	48.723	-0.099	49.196	1.00	17.41
2839	CB	ILE	A	483	49.000	2.569	47.120	1.00	14.77
2840	CG1	ILE	A	483	50.358	2.717	47.833	1.00	15.86
2841	CG2	ILE	A	483	48.429	3.967	46.809	1.00	15.27
2842	CD1	ILE	A	483	51.356	1.531	47.671	1.00	13.17
2843	N	THR	A	484	48.308	-0.555	47.050	1.00	15.28
2844	CA	THR	A	484	48.633	-1.952	47.213	1.00	15.28
2845	C	THR	A	484	49.933	-2.359	46.538	1.00	15.86
2846	O	THR	A	484	50.410	-3.469	46.796	1.00	13.72
2847	CB	THR	A	484	47.549	-2.863	46.532	1.00	16.48
2848	OG1	THR	A	484	47.638	-2.693	45.102	1.00	16.43
2849	CG2	THR	A	484	46.150	-2.505	47.003	1.00	16.06
2850	N	THR	A	485	50.443	-1.551	45.605	1.00	14.91
2851	CA	THR	A	485	51.595	-1.965	44.783	1.00	15.42
2852	C	THR	A	485	52.427	-0.757	44.384	1.00	15.53
2853	O	THR	A	485	51.863	0.244	43.919	1.00	15.10
2854	CB	THR	A	485	51.065	-2.655	43.513	1.00	15.83
2855	OG1	THR	A	485	50.004	-3.584	43.802	1.00	16.38
2856	CG2	THR	A	485	52.059	-3.489	42.695	1.00	16.14
2857	N	VAL	A	486	53.764	-0.790	44.555	1.00	14.94
2858	CA	VAL	A	486	54.652	0.297	44.134	1.00	12.74
2859	C	VAL	A	486	55.245	0.001	42.748	1.00	14.15
2860	O	VAL	A	486	55.788	-1.134	42.601	1.00	14.85
2861	CB	VAL	A	486	55.857	0.483	45.082	1.00	14.01
2862	CG1	VAL	A	486	56.783	1.610	44.531	1.00	12.76
2863	CG2	VAL	A	486	55.303	0.961	46.438	1.00	15.43
2864	N	GLN	A	487	55.159	0.899	41.798	1.00	12.39
2865	CA	GLN	A	487	55.823	0.699	40.507	1.00	13.69
2866	C	GLN	A	487	57.124	1.507	40.520	1.00	14.02
2867	O	GLN	A	487	57.008	2.717	40.530	1.00	15.37
2868	CB	GLN	A	487	54.975	1.132	39.304	1.00	14.53
2869	CG	GLN	A	487	55.555	0.810	37.899	1.00	14.85
2870	CD	GLN	A	487	54.658	1.489	36.844	1.00	15.25
2871	OE1	GLN	A	487	53.542	0.999	36.600	1.00	12.63
2872	NE2	GLN	A	487	55.086	2.600	36.263	1.00	14.69
2873	N	LEU	A	488	58.291	0.856	40.520	1.00	13.77
2874	CA	LEU	A	488	59.537	1.560	40.518	1.00	15.79
2875	C	LEU	A	488	60.035	1.987	39.152	1.00	15.05
2876	O	LEU	A	488	60.073	1.122	38.294	1.00	15.87
2877	CB	LEU	A	488	60.695	0.684	41.146	1.00	14.51

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2878	CG	LEU	A	488	60.575	0.236	42.618	1.00	16.06
2879	CD1	LEU	A	488	61.575	-0.885	42.971	1.00	15.85
2880	CD2	LEU	A	488	60.742	1.336	43.642	1.00	11.74
2881	N	GLN	A	489	60.487	3.246	39.045	1.00	15.31
2882	CA	GLN	A	489	61.188	3.679	37.812	1.00	14.87
2883	C	GLN	A	489	62.425	2.807	37.665	1.00	14.33
2884	O	GLN	A	489	62.859	2.155	38.606	1.00	14.60
2885	CB	GLN	A	489	61.403	5.188	37.805	1.00	15.88
2886	CG	GLN	A	489	60.080	5.982	37.617	1.00	16.42
2887	CD	GLN	A	489	60.312	7.400	37.152	1.00	16.75
2888	OE1	GLN	A	489	60.684	7.691	35.982	1.00	19.64
2889	NE2	GLN	A	489	60.177	8.368	38.027	1.00	14.55
2890	N	PRO	A	490	63.045	2.689	36.494	1.00	14.20
2891	CA	PRO	A	490	64.089	1.703	36.225	1.00	13.53
2892	C	PRO	A	490	65.155	1.438	37.241	1.00	14.81
2893	O	PRO	A	490	65.895	2.388	37.605	1.00	15.34
2894	CB	PRO	A	490	64.707	2.269	34.906	1.00	13.82
2895	CG	PRO	A	490	63.479	2.776	34.197	1.00	15.17
2896	CD	PRO	A	490	62.691	3.502	35.299	1.00	11.82
2897	N	VAL	A	491	65.280	0.210	37.709	1.00	14.57
2898	CA	VAL	A	491	66.362	-0.156	38.655	1.00	16.33
2899	C	VAL	A	491	67.293	-1.160	37.970	1.00	17.32
2900	O	VAL	A	491	68.202	-1.714	38.584	1.00	17.98
2901	CB	VAL	A	491	65.792	-0.718	39.976	1.00	15.46
2902	CG1	VAL	A	491	64.974	0.369	40.708	1.00	13.55
2903	CG2	VAL	A	491	64.915	-1.944	39.688	1.00	14.62
2904	N	GLU	A	492	67.092	-1.504	36.697	1.00	18.44
2905	CA	GLU	A	492	68.031	-2.245	35.863	1.00	16.40
2906	C	GLU	A	492	69.156	-1.271	35.451	1.00	17.63
2907	O	GLU	A	492	68.937	-0.141	34.964	1.00	15.32
2908	CB	GLU	A	492	67.459	-2.927	34.598	1.00	15.59
2909	CG	GLU	A	492	66.412	-4.003	34.981	1.00	16.27
2910	CD	GLU	A	492	65.731	-4.713	33.824	1.00	16.24
2911	OE1	GLU	A	492	65.079	-5.765	33.984	1.00	15.93
2912	OE2	GLU	A	492	65.871	-4.235	32.678	1.00	16.98
2913	N	GLU	A	493	70.400	-1.716	35.653	1.00	17.89
2914	CA	GLU	A	493	71.592	-0.901	35.413	1.00	18.19
2915	C	GLU	A	493	71.592	-0.092	34.107	1.00	17.67
2916	O	GLU	A	493	71.579	-0.640	33.012	1.00	15.24
2917	CB	GLU	A	493	72.869	-1.773	35.447	1.00	18.34
2918	CG	GLU	A	493	74.173	-1.020	35.230	1.00	18.92
2919	CD	GLU	A	493	74.742	-0.344	36.455	1.00	19.23
2920	OE1	GLU	A	493	75.796	0.334	36.325	1.00	17.41
2921	OE2	GLU	A	493	74.095	-0.479	37.541	1.00	19.62
2922	N	PHE	A	494	71.755	1.230	34.238	1.00	15.08
2923	CA	PHE	A	494	71.716	2.064	33.051	1.00	17.22
2924	C	PHE	A	494	73.040	2.834	32.904	1.00	17.93
2925	O	PHE	A	494	73.846	2.871	33.840	1.00	17.61
2926	CB	PHE	A	494	70.494	2.985	33.079	1.00	15.05
2927	CG	PHE	A	494	70.209	3.732	34.347	1.00	13.69
2928	CD1	PHE	A	494	69.309	3.238	35.283	1.00	13.97
2929	CD2	PHE	A	494	70.814	4.964	34.603	1.00	14.09
2930	CE1	PHE	A	494	69.008	3.927	36.442	1.00	13.34
2931	CE2	PHE	A	494	70.548	5.662	35.766	1.00	13.82
2932	CZ	PHE	A	494	69.650	5.128	36.706	1.00	14.68
2933	N	ASN	A	495	73.262	3.489	31.758	1.00	17.56
2934	CA	ASN	A	495	74.549	4.074	31.443	1.00	19.21
2935	C	ASN	A	495	74.759	5.505	31.926	1.00	18.67
2936	O	ASN	A	495	75.915	5.887	32.059	1.00	17.87
2937	CB	ASN	A	495	74.850	4.084	29.931	1.00	17.20
2938	CG	ASN	A	495	76.266	4.473	29.570	1.00	20.20
2939	OD1	ASN	A	495	77.257	3.802	29.891	1.00	18.77
2940	ND2	ASN	A	495	76.482	5.618	28.938	1.00	19.57
2941	N	SER	A	496	73.715	6.299	32.041	1.00	17.59
2942	CA	SER	A	496	73.827	7.723	32.297	1.00	17.54
2943	C	SER	A	496	74.342	8.127	33.652	1.00	18.68
2944	O	SER	A	496	74.638	9.331	33.798	1.00	18.94
2945	CB	SER	A	496	72.487	8.433	32.001	1.00	19.07
2946	OG	SER	A	496	71.377	7.889	32.711	1.00	17.68
2947	N	ILE	A	497	74.441	7.273	34.670	1.00	16.74
2948	CA	ILE	A	497	75.071	7.777	35.908	1.00	17.05
2949	C	ILE	A	497	76.434	7.104	36.029	1.00	17.86
2950	O	ILE	A	497	76.528	5.880	35.928	1.00	16.60
2951	CB	ILE	A	497	74.203	7.473	37.156	1.00	18.85
2952	CG1	ILE	A	497	72.950	8.366	37.145	1.00	18.39
2953	CG2	ILE	A	497	75.033	7.586	38.435	1.00	16.11
2954	CD1	ILE	A	497	71.845	8.001	38.145	1.00	18.90
2955	N	ASP	A	498	77.478	7.888	36.227	1.00	18.34
2956	CA	ASP	A	498	78.806	7.346	36.522	1.00	19.14
2957	C	ASP	A	498	78.770	6.898	37.971	1.00	17.01
2958	O	ASP	A	498	78.609	7.762	38.858	1.00	15.12
2959	CB	ASP	A	498	79.861	8.458	36.364	1.00	21.90
2960	CG	ASP	A	498	81.295	8.069	36.759	1.00	24.10
2961	OD1	ASP	A	498	82.155	8.832	36.229	1.00	23.49
2962	OD2	ASP	A	498	81.615	7.096	37.480	1.00	19.87
2963	N	GLU	A	499	79.011	5.646	38.280	1.00	16.55
2964	CA	GLU	A	499	78.977	5.108	39.632	1.00	19.92
2965	C	GLU	A	499	79.988	5.691	40.614	1.00	21.17
2966	O	GLU	A	499	79.775	5.543	41.836	1.00	20.23
2967	CB	GLU	A	499	79.090	3.565	39.610	1.00	18.52
2968	CG	GLU	A	499	77.783	3.044	38.948	1.00	17.11
2969	CD	GLU	A	499	77.715	1.561	38.901	1.00	19.30
2970	OE1	GLU	A	499	78.782	0.866	38.946	1.00	18.97
2971	OE2	GLU	A	499	76.609	0.973	38.775	1.00	18.01
2972	N	THR	A	500	81.008	6.404	40.126	1.00	20.80
2973	CA	THR	A	500	81.940	7.053	41.057	1.00	23.34

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2974	C	THR	A	500	81.372	8.400	41.497	1.00	24.20
2975	O	THR	A	500	82.015	9.077	42.287	1.00	24.37
2976	CB	THR	A	500	83.342	7.317	40.473	1.00	21.92
2977	OG1	THR	A	500	83.230	8.244	39.379	1.00	20.76
2978	CG2	THR	A	500	84.023	6.044	39.986	1.00	22.58
2979	N	GLN	A	501	80.313	8.895	40.895	1.00	26.63
2980	CA	GLN	A	501	79.580	10.111	41.217	1.00	29.35
2981	C	GLN	A	501	78.081	9.780	41.293	1.00	29.18
2982	O	GLN	A	501	77.286	10.114	40.421	1.00	28.10
2983	CB	GLN	A	501	79.695	11.145	40.089	1.00	32.33
2984	CG	GLN	A	501	81.113	11.471	39.637	1.00	36.70
2985	CD	GLN	A	501	81.850	12.239	40.710	1.00	41.32
2986	OE1	GLN	A	501	81.235	12.619	41.723	1.00	43.52
2987	NE2	GLN	A	501	83.153	12.497	40.515	1.00	44.21
2988	N	PRO	A	502	77.652	9.030	42.297	1.00	29.53
2989	CA	PRO	A	502	76.292	8.507	42.359	1.00	28.54
2990	C	PRO	A	502	75.175	9.471	42.670	1.00	28.87
2991	O	PRO	A	502	74.004	9.050	42.701	1.00	30.15
2992	CB	PRO	A	502	76.406	7.392	43.399	1.00	26.18
2993	CG	PRO	A	502	77.510	7.853	44.309	1.00	27.23
2994	CD	PRO	A	502	78.477	8.622	43.471	1.00	27.08
2995	N	ASP	A	503	75.432	10.751	42.881	1.00	28.94
2996	CA	ASP	A	503	74.380	11.709	43.179	1.00	29.84
2997	C	ASP	A	503	73.930	12.521	41.976	1.00	28.92
2998	O	ASP	A	503	73.125	13.446	42.132	1.00	30.62
2999	CB	ASP	A	503	74.783	12.642	44.344	1.00	29.97
3000	CG	ASP	A	503	74.845	11.877	45.654	1.00	31.52
3001	OD1	ASP	A	503	74.016	10.975	45.912	1.00	29.14
3002	OD2	ASP	A	503	75.783	12.160	46.439	1.00	33.43
3003	N	THR	A	504	74.384	12.204	40.790	1.00	28.14
3004	CA	THR	A	504	73.894	12.795	39.547	1.00	28.02
3005	C	THR	A	504	72.464	12.303	39.332	1.00	25.44
3006	O	THR	A	504	72.090	11.307	39.988	1.00	26.41
3007	CB	THR	A	504	74.817	12.287	38.421	1.00	30.26
3008	OG1	THR	A	504	74.365	12.697	37.137	1.00	34.86
3009	CG2	THR	A	504	74.853	10.784	38.452	1.00	32.35
3010	N	TYR	A	505	71.617	12.976	38.574	1.00	22.48
3011	CA	TYR	A	505	70.198	12.564	38.498	1.00	20.51
3012	C	TYR	A	505	69.839	11.991	37.135	1.00	20.40
3013	O	TYR	A	505	70.037	12.679	36.103	1.00	19.81
3014	CB	TYR	A	505	69.281	13.777	38.795	1.00	19.30
3015	CG	TYR	A	505	67.814	13.347	38.862	1.00	19.19
3016	CD1	TYR	A	505	67.241	13.027	40.115	1.00	17.54
3017	CD2	TYR	A	505	67.023	13.226	37.730	1.00	16.46
3018	CE1	TYR	A	505	65.931	12.559	40.199	1.00	16.03
3019	CE2	TYR	A	505	65.697	12.777	37.831	1.00	16.62
3020	CZ	TYR	A	505	65.163	12.442	39.058	1.00	17.37
3021	OH	TYR	A	505	63.859	11.975	39.132	1.00	16.33
3022	N	ASN	A	506	69.117	10.864	37.112	1.00	19.02
3023	CA	ASN	A	506	68.525	10.394	35.854	1.00	17.54
3024	C	ASN	A	506	67.354	9.433	36.132	1.00	16.94
3025	O	ASN	A	506	67.448	8.585	37.023	1.00	15.04
3026	CB	ASN	A	506	69.538	9.697	34.935	1.00	17.11
3027	CG	ASN	A	506	69.102	9.692	33.481	1.00	19.56
3028	OD1	ASN	A	506	68.263	8.880	33.019	1.00	18.08
3029	ND2	ASN	A	506	69.679	10.641	32.729	1.00	18.09
3030	N	TRP	A	507	66.363	9.479	35.216	1.00	14.78
3031	CA	TRP	A	507	65.263	8.515	35.282	1.00	14.79
3032	C	TRP	A	507	65.716	7.096	34.995	1.00	14.58
3033	O	TRP	A	507	65.101	6.151	35.466	1.00	12.62
3034	CB	TRP	A	507	64.189	8.879	34.236	1.00	13.89
3035	CG	TRP	A	507	63.208	9.944	34.647	1.00	13.96
3036	CD1	TRP	A	507	63.021	10.504	35.878	1.00	13.86
3037	CD2	TRP	A	507	62.268	10.598	33.765	1.00	13.76
3038	NE1	TRP	A	507	62.035	11.509	35.797	1.00	14.63
3039	CE2	TRP	A	507	61.572	11.557	34.520	1.00	14.09
3040	CE3	TRP	A	507	62.006	10.488	32.396	1.00	14.36
3041	CZ2	TRP	A	507	60.623	12.410	33.943	1.00	15.35
3042	CZ3	TRP	A	507	61.039	11.314	31.837	1.00	16.79
3043	CH2	TRP	A	507	60.359	12.283	32.620	1.00	14.29
3044	N	GLY	A	508	66.779	6.933	34.176	1.00	14.06
3045	CA	GLY	A	508	67.280	5.621	33.845	1.00	14.97
3046	C	GLY	A	508	66.688	4.906	32.664	1.00	14.99
3047	O	GLY	A	508	66.794	3.661	32.610	1.00	13.65
3048	N	TYR	A	509	66.161	5.623	31.664	1.00	15.66
3049	CA	TYR	A	509	65.673	5.037	30.419	1.00	16.40
3050	C	TYR	A	509	66.771	4.746	29.389	1.00	16.91
3051	O	TYR	A	509	66.436	4.451	28.241	1.00	16.03
3052	CB	TYR	A	509	64.471	5.812	29.758	1.00	14.79
3053	CG	TYR	A	509	63.288	5.731	30.729	1.00	17.63
3054	CD1	TYR	A	509	62.469	4.608	30.816	1.00	15.29
3055	CD2	TYR	A	509	63.037	6.779	31.616	1.00	17.85
3056	CE1	TYR	A	509	61.434	4.549	31.726	1.00	14.88
3057	CE2	TYR	A	509	62.012	6.715	32.540	1.00	17.47
3058	CZ	TYR	A	509	61.210	5.585	32.587	1.00	18.26
3059	OH	TYR	A	509	60.204	5.532	33.541	1.00	18.82
3060	N	ASP	A	510	68.021	4.495	29.735	1.00	16.31
3061	CA	ASP	A	510	69.142	4.129	28.870	1.00	18.35
3062	C	ASP	A	510	69.891	2.912	29.392	1.00	17.34
3063	O	ASP	A	510	71.041	2.945	29.873	1.00	20.99
3064	CB	ASP	A	510	70.120	5.322	28.723	1.00	19.25
3065	CG	ASP	A	510	70.746	5.804	30.000	1.00	21.01
3066	OD1	ASP	A	510	70.057	5.942	31.032	1.00	21.87
3067	OD2	ASP	A	510	71.991	6.068	30.056	1.00	23.52
3068	N	PRO	A	511	69.294	1.752	29.370	1.00	16.56
3069	CA	PRO	A	511	69.789	0.507	29.915	1.00	17.26

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3070	C	PRO	A	511	71.112	0.019	29.272	1.00	17.06
3071	O	PRO	A	511	71.327	0.259	28.077	1.00	16.16
3072	CB	PRO	A	511	68.730	-0.564	29.675	1.00	16.53
3073	CG	PRO	A	511	67.898	-0.001	28.531	1.00	17.61
3074	CD	PRO	A	511	67.914	1.498	28.752	1.00	17.12
3075	N	ARG	A	512	71.925	-0.624	30.102	1.00	16.69
3076	CA	ARG	A	512	73.212	-1.174	29.634	1.00	16.56
3077	C	ARG	A	512	73.392	-2.618	30.065	1.00	16.11
3078	O	ARG	A	512	73.824	-3.472	29.278	1.00	16.43
3079	CB	ARG	A	512	74.394	-0.275	30.088	1.00	18.15
3080	CG	ARG	A	512	75.778	-0.703	29.616	1.00	18.63
3081	CD	ARG	A	512	76.929	0.127	30.219	1.00	19.47
3082	NE	ARG	A	512	77.011	-0.045	31.687	1.00	20.90
3083	CZ	ARG	A	512	77.354	0.937	32.563	1.00	20.85
3084	NH1	ARG	A	512	77.328	0.708	33.877	1.00	20.82
3085	NH2	ARG	A	512	77.653	2.184	32.233	1.00	19.17
3086	N	ASN	A	513	73.175	-2.970	31.326	1.00	15.21
3087	CA	ASN	A	513	73.323	-4.307	31.896	1.00	14.14
3088	C	ASN	A	513	71.957	-4.696	32.471	1.00	15.83
3089	O	ASN	A	513	71.562	-4.414	33.623	1.00	14.75
3090	CB	ASN	A	513	74.425	-4.304	32.991	1.00	13.68
3091	CG	ASN	A	513	75.722	-3.670	32.503	1.00	15.65
3092	OD1	ASN	A	513	75.960	-2.463	32.702	1.00	13.93
3093	ND2	ASN	A	513	76.592	-4.443	31.817	1.00	13.93
3094	N	TYR	A	514	71.137	-5.398	31.687	1.00	16.49
3095	CA	TYR	A	514	69.742	-5.666	32.068	1.00	17.77
3096	C	TYR	A	514	69.496	-6.572	33.280	1.00	18.89
3097	O	TYR	A	514	68.398	-6.564	33.865	1.00	16.26
3098	CB	TYR	A	514	69.017	-6.266	30.861	1.00	18.16
3099	CG	TYR	A	514	68.726	-5.341	29.689	1.00	18.97
3100	CD1	TYR	A	514	67.565	-4.560	29.672	1.00	18.42
3101	CD2	TYR	A	514	69.604	-5.279	28.597	1.00	19.59
3102	CE1	TYR	A	514	67.289	-3.734	28.595	1.00	18.29
3103	CE2	TYR	A	514	69.328	-4.444	27.514	1.00	19.38
3104	CZ	TYR	A	514	68.167	-3.696	27.521	1.00	19.34
3105	OH	TYR	A	514	67.857	-2.887	26.450	1.00	22.29
3106	N	ASN	A	515	70.493	-7.389	33.643	1.00	17.63
3107	CA	ASN	A	515	70.280	-8.339	34.745	1.00	17.34
3108	C	ASN	A	515	70.978	-7.906	36.018	1.00	17.54
3109	O	ASN	A	515	71.187	-8.752	36.913	1.00	18.12
3110	CB	ASN	A	515	70.786	-9.703	34.185	1.00	16.85
3111	CG	ASN	A	515	69.974	-10.095	32.944	1.00	18.64
3112	OD1	ASN	A	515	70.465	-10.350	31.826	1.00	21.03
3113	ND2	ASN	A	515	68.680	-10.119	33.147	1.00	11.82
3114	N	VAL	A	516	71.402	-6.661	36.141	1.00	14.31
3115	CA	VAL	A	516	72.083	-6.138	37.344	1.00	15.74
3116	C	VAL	A	516	71.301	-4.960	37.911	1.00	16.74
3117	O	VAL	A	516	70.892	-4.053	37.176	1.00	16.35
3118	CB	VAL	A	516	73.478	-5.606	36.838	1.00	16.38
3119	CG1	VAL	A	516	74.289	-4.915	37.924	1.00	15.90
3120	CG2	VAL	A	516	74.293	-6.720	36.163	1.00	15.48
3121	N	PRO	A	517	71.121	-4.832	39.223	1.00	17.59
3122	CA	PRO	A	517	70.522	-3.663	39.846	1.00	15.46
3123	C	PRO	A	517	71.370	-2.408	39.664	1.00	16.15
3124	O	PRO	A	517	72.601	-2.451	39.870	1.00	17.59
3125	CB	PRO	A	517	70.481	-4.030	41.330	1.00	16.03
3126	CG	PRO	A	517	70.630	-5.532	41.363	1.00	16.94
3127	CD	PRO	A	517	71.656	-5.777	40.261	1.00	15.72
3128	N	GLU	A	518	70.756	-1.245	39.475	1.00	13.80
3129	CA	GLU	A	518	71.457	0.025	39.340	1.00	15.14
3130	C	GLU	A	518	72.366	0.288	40.567	1.00	15.73
3131	O	GLU	A	518	71.844	0.352	41.694	1.00	14.71
3132	CB	GLU	A	518	70.444	1.149	39.065	1.00	14.95
3133	CG	GLU	A	518	71.065	2.558	39.118	1.00	15.19
3134	CD	GLU	A	518	72.139	2.790	38.080	1.00	17.66
3135	OE1	GLU	A	518	72.129	2.189	36.974	1.00	16.65
3136	OE2	GLU	A	518	73.093	3.591	38.350	1.00	17.95
3137	N	GLY	A	519	73.671	0.589	40.305	1.00	15.19
3138	CA	GLY	A	519	74.567	0.786	41.499	1.00	15.74
3139	C	GLY	A	519	74.412	2.112	42.221	1.00	15.83
3140	O	GLY	A	519	74.575	2.196	43.455	1.00	14.13
3141	N	ALA	A	520	73.905	3.163	41.577	1.00	16.04
3142	CA	ALA	A	520	73.780	4.471	42.239	1.00	18.29
3143	C	ALA	A	520	72.771	4.499	43.381	1.00	18.95
3144	O	ALA	A	520	72.856	5.422	44.196	1.00	16.80
3145	CB	ALA	A	520	73.427	5.513	41.206	1.00	18.41
3146	N	TYR	A	521	71.811	3.561	43.410	1.00	17.07
3147	CA	TYR	A	521	70.819	3.494	44.486	1.00	16.73
3148	C	TYR	A	521	71.260	2.579	45.612	1.00	17.27
3149	O	TYR	A	521	70.528	2.470	46.610	1.00	17.61
3150	CB	TYR	A	521	69.446	3.021	43.941	1.00	17.24
3151	CG	TYR	A	521	68.942	3.859	42.764	1.00	15.38
3152	CD1	TYR	A	521	69.117	5.247	42.743	1.00	15.18
3153	CD2	TYR	A	521	68.284	3.264	41.724	1.00	15.31
3154	CE1	TYR	A	521	68.738	6.002	41.655	1.00	16.88
3155	CE2	TYR	A	521	67.798	4.003	40.641	1.00	16.48
3156	CZ	TYR	A	521	68.057	5.367	40.617	1.00	17.62
3157	OH	TYR	A	521	67.606	6.097	39.531	1.00	19.26
3158	N	ALA	A	522	72.417	1.907	45.435	1.00	17.17
3159	CA	ALA	A	522	72.945	1.042	46.518	1.00	15.89
3160	C	ALA	A	522	73.921	1.876	47.348	1.00	15.60
3161	O	ALA	A	522	74.342	2.981	46.946	1.00	17.19
3162	CB	ALA	A	522	73.659	-0.164	45.905	1.00	13.85
3163	N	THR	A	523	74.102	1.561	48.625	1.00	15.78
3164	CA	THR	A	523	75.072	2.230	49.489	1.00	17.82
3165	C	THR	A	523	76.470	1.956	48.944	1.00	18.92

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3166	O	THR	A	523	77.211	2.947	49.304	1.00	17.26
3167	CB	THR	A	523	74.948	1.890	50.976	1.00	17.94
3168	OG1	THR	A	523	75.385	0.524	51.116	1.00	17.69
3169	CG2	THR	A	523	73.506	2.011	51.516	1.00	16.78
3170	N	THR	A	524	76.940	1.218	48.019	1.00	16.59
3171	CA	THR	A	524	78.214	1.239	47.375	1.00	17.47
3172	C	THR	A	524	77.987	0.549	46.014	1.00	15.97
3173	O	THR	A	524	77.245	-0.434	46.035	1.00	15.00
3174	CB	THR	A	524	79.381	0.537	48.089	1.00	16.77
3175	OG1	THR	A	524	80.598	0.447	47.315	1.00	18.09
3176	CG2	THR	A	524	79.009	-0.895	48.485	1.00	17.48
3177	N	PRO	A	525	78.671	0.941	44.975	1.00	16.83
3178	CA	PRO	A	525	78.667	0.231	43.696	1.00	16.43
3179	C	PRO	A	525	79.532	-1.019	43.697	1.00	17.20
3180	O	PRO	A	525	79.479	-1.868	42.773	1.00	16.05
3181	CB	PRO	A	525	79.261	1.241	42.734	1.00	17.75
3182	CG	PRO	A	525	80.236	2.061	43.551	1.00	17.07
3183	CD	PRO	A	525	79.581	2.153	44.935	1.00	16.46
3184	N	GLU	A	526	80.334	-1.296	44.754	1.00	17.68
3185	CA	GLU	A	526	81.242	-2.413	44.797	1.00	15.57
3186	C	GLU	A	526	80.552	-3.755	45.025	1.00	18.65
3187	O	GLU	A	526	79.678	-3.828	45.910	1.00	17.57
3188	CB	GLU	A	526	82.241	-2.286	45.993	1.00	18.74
3189	CG	GLU	A	526	83.196	-1.098	45.920	1.00	17.93
3190	CD	GLU	A	526	84.240	-1.354	44.831	1.00	20.14
3191	OE1	GLU	A	526	84.455	-2.518	44.447	1.00	18.35
3192	OE2	GLU	A	526	84.830	-0.361	44.367	1.00	20.55
3193	N	GLY	A	527	80.932	-4.816	44.303	1.00	16.41
3194	CA	GLY	A	527	80.349	-6.100	44.587	1.00	18.62
3195	C	GLY	A	527	78.868	-6.310	44.654	1.00	19.21
3196	O	GLY	A	527	78.114	-5.715	43.903	1.00	19.86
3197	N	THR	A	528	78.364	-7.119	45.605	1.00	20.27
3198	CA	THR	A	528	76.950	-7.510	45.574	1.00	18.39
3199	C	THR	A	528	76.092	-6.707	46.515	1.00	19.42
3200	O	THR	A	528	74.938	-7.063	46.774	1.00	18.50
3201	CB	THR	A	528	76.855	-9.024	45.904	1.00	18.15
3202	OG1	THR	A	528	77.414	-9.233	47.211	1.00	20.44
3203	CG2	THR	A	528	77.688	-9.855	44.941	1.00	17.77
3204	N	ALA	A	529	76.662	-5.642	47.063	1.00	18.16
3205	CA	ALA	A	529	75.933	-4.712	47.906	1.00	18.05
3206	C	ALA	A	529	74.630	-4.330	47.203	1.00	18.52
3207	O	ALA	A	529	73.580	-4.348	47.859	1.00	16.31
3208	CB	ALA	A	529	76.703	-3.413	48.157	1.00	18.09
3209	N	ARG	A	530	74.624	-4.063	45.907	1.00	17.37
3210	CA	ARG	A	530	73.422	-3.669	45.184	1.00	16.22
3211	C	ARG	A	530	72.334	-4.739	45.116	1.00	16.28
3212	O	ARG	A	530	71.148	-4.377	45.045	1.00	15.45
3213	CB	ARG	A	530	73.783	-3.225	43.762	1.00	15.05
3214	CG	ARG	A	530	74.440	-4.346	42.940	1.00	16.74
3215	CD	ARG	A	530	74.961	-3.751	41.630	1.00	14.90
3216	NE	ARG	A	530	76.197	-2.937	41.763	1.00	15.63
3217	CZ	ARG	A	530	76.515	-2.064	40.802	1.00	15.30
3218	NH1	ARG	A	530	77.670	-1.407	40.853	1.00	17.75
3219	NH2	ARG	A	530	75.706	-1.836	39.773	1.00	12.09
3220	N	ILE	A	531	72.700	-6.005	45.108	1.00	14.54
3221	CA	ILE	A	531	71.804	-7.113	45.021	1.00	17.37
3222	C	ILE	A	531	71.001	-7.347	46.318	1.00	18.65
3223	O	ILE	A	531	69.754	-7.487	46.311	1.00	14.76
3224	CB	ILE	A	531	72.556	-8.391	44.601	1.00	17.38
3225	CG1	ILE	A	531	73.146	-8.298	43.182	1.00	17.59
3226	CG2	ILE	A	531	71.624	-9.601	44.601	1.00	16.93
3227	CD1	ILE	A	531	73.965	-9.553	42.804	1.00	16.77
3228	N	THR	A	532	71.717	-7.408	47.426	1.00	16.30
3229	CA	THR	A	532	71.120	-7.596	48.745	1.00	17.14
3230	C	THR	A	532	70.203	-6.408	49.093	1.00	16.96
3231	O	THR	A	532	69.122	-6.670	49.634	1.00	17.94
3232	CB	THR	A	532	72.202	-7.696	49.838	1.00	18.30
3233	OG1	THR	A	532	73.048	-8.840	49.519	1.00	17.90
3234	CG2	THR	A	532	71.578	-7.989	51.205	1.00	15.71
3235	N	GLU	A	533	70.608	-5.180	48.808	1.00	13.67
3236	CA	GLU	A	533	69.821	-3.993	49.110	1.00	15.12
3237	C	GLU	A	533	68.532	-3.891	48.317	1.00	16.63
3238	O	GLU	A	533	67.551	-3.400	48.903	1.00	14.08
3239	CB	GLU	A	533	70.707	-2.740	49.008	1.00	16.01
3240	CG	GLU	A	533	71.682	-2.653	50.183	1.00	17.57
3241	CD	GLU	A	533	72.716	-1.580	50.093	1.00	19.20
3242	OE1	GLU	A	533	73.811	-1.717	50.714	1.00	21.48
3243	OE2	GLU	A	533	72.475	-0.536	49.428	1.00	20.43
3244	N	LEU	A	534	68.465	-4.294	47.052	1.00	14.75
3245	CA	LEU	A	534	67.179	-4.230	46.320	1.00	14.76
3246	C	LEU	A	534	66.255	-5.331	46.838	1.00	13.97
3247	O	LEU	A	534	65.040	-5.162	46.998	1.00	13.22
3248	CB	LEU	A	534	67.451	-4.277	44.804	1.00	11.25
3249	CG	LEU	A	534	66.205	-4.408	43.904	1.00	13.31
3250	CD1	LEU	A	534	65.165	-3.291	44.168	1.00	10.17
3251	CD2	LEU	A	534	66.721	-4.308	42.454	1.00	10.59
3252	N	LYS	A	535	66.805	-6.516	47.087	1.00	13.87
3253	CA	LYS	A	535	66.086	-7.618	47.715	1.00	15.88
3254	C	LYS	A	535	65.530	-7.196	49.082	1.00	16.79
3255	O	LYS	A	535	64.377	-7.547	49.376	1.00	17.52
3256	CB	LYS	A	535	66.887	-8.917	47.860	1.00	15.40
3257	CG	LYS	A	535	67.402	-9.601	46.617	1.00	18.60
3258	CD	LYS	A	535	68.119	-10.918	46.903	1.00	17.82
3259	CE	LYS	A	535	68.558	-11.541	45.575	1.00	18.33
3260	NZ	LYS	A	535	69.546	-12.644	45.766	1.00	16.36
3261	N	GLN	A	536	66.207	-6.389	49.915	1.00	16.15

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3262	CA	GLN	A	536	65.663	-5.931	51.188	1.00	17.43
3263	C	GLN	A	536	64.484	-4.948	51.011	1.00	15.85
3264	O	GLN	A	536	63.556	-4.932	51.829	1.00	13.29
3265	CB	GLN	A	536	66.735	-5.260	52.068	1.00	16.73
3266	CG	GLN	A	536	67.783	-6.230	52.583	1.00	20.31
3267	CD	GLN	A	536	68.982	-5.556	53.221	1.00	22.94
3268	OE1	GLN	A	536	69.836	-4.925	52.614	1.00	21.17
3269	NE2	GLN	A	536	69.036	-5.681	54.536	1.00	25.61
3270	N	LEU	A	537	64.505	-4.105	49.992	1.00	16.38
3271	CA	LEU	A	537	63.425	-3.174	49.650	1.00	16.60
3272	C	LEU	A	537	62.179	-4.051	49.336	1.00	17.04
3273	O	LEU	A	537	61.080	-3.702	49.797	1.00	16.16
3274	CB	LEU	A	537	63.756	-2.314	48.435	1.00	17.59
3275	CG	LEU	A	537	62.757	-1.314	47.829	1.00	15.05
3276	CD1	LEU	A	537	63.348	-0.200	46.975	1.00	16.00
3277	CD2	LEU	A	537	61.771	-2.134	46.970	1.00	15.65
3278	N	ILE	A	538	62.361	-5.013	48.468	1.00	16.09
3279	CA	ILE	A	538	61.288	-5.922	48.067	1.00	16.51
3280	C	ILE	A	538	60.701	-6.677	49.245	1.00	17.89
3281	O	ILE	A	538	59.479	-6.811	49.400	1.00	16.47
3282	CB	ILE	A	538	61.777	-6.836	46.920	1.00	16.94
3283	CG1	ILE	A	538	62.083	-5.982	45.686	1.00	14.36
3284	CG2	ILE	A	538	60.667	-7.886	46.675	1.00	17.13
3285	CD1	ILE	A	538	62.805	-6.628	44.509	1.00	13.95
3286	N	GLN	A	539	61.538	-7.186	50.141	1.00	16.57
3287	CA	GLN	A	539	61.128	-7.943	51.314	1.00	17.53
3288	C	GLN	A	539	60.345	-7.077	52.312	1.00	18.11
3289	O	GLN	A	539	59.366	-7.553	52.893	1.00	17.99
3290	CB	GLN	A	539	62.351	-8.523	52.027	1.00	19.31
3291	CG	GLN	A	539	62.149	-9.256	53.324	1.00	19.71
3292	CD	GLN	A	539	63.417	-9.837	53.936	1.00	20.54
3293	OE1	GLN	A	539	64.431	-9.149	54.033	1.00	22.88
3294	NE2	GLN	A	539	63.404	-11.074	54.356	1.00	19.77
3295	N	SER	A	540	60.765	-5.844	52.489	1.00	18.42
3296	CA	SER	A	540	60.102	-4.916	53.403	1.00	20.34
3297	C	SER	A	540	58.723	-4.480	52.906	1.00	20.30
3298	O	SER	A	540	57.763	-4.529	53.714	1.00	16.87
3299	CB	SER	A	540	61.125	-3.801	53.586	1.00	21.39
3300	OG	SER	A	540	60.542	-2.651	54.113	1.00	26.78
3301	N	LEU	A	541	58.502	-4.242	51.613	1.00	17.30
3302	CA	LEU	A	541	57.127	-3.909	51.140	1.00	18.58
3303	C	LEU	A	541	56.231	-5.132	51.270	1.00	18.04
3304	O	LEU	A	541	55.047	-5.034	51.690	1.00	17.70
3305	CB	LEU	A	541	57.128	-3.311	49.731	1.00	19.55
3306	CG	LEU	A	541	57.908	-2.022	49.522	1.00	20.99
3307	CD1	LEU	A	541	58.100	-1.486	48.104	1.00	20.76
3308	CD2	LEU	A	541	57.190	-0.836	50.210	1.00	21.46
3309	N	HIS	A	542	56.739	-6.322	50.902	1.00	15.72
3310	CA	HIS	A	542	55.993	-7.545	50.990	1.00	17.12
3311	C	HIS	A	542	55.499	-7.790	52.421	1.00	20.37
3312	O	HIS	A	542	54.326	-8.187	52.598	1.00	17.99
3313	CB	HIS	A	542	56.747	-8.783	50.476	1.00	17.02
3314	CG	HIS	A	542	56.882	-8.831	48.975	1.00	16.64
3315	ND1	HIS	A	542	57.700	-9.780	48.377	1.00	15.29
3316	CD2	HIS	A	542	56.349	-8.154	47.933	1.00	14.04
3317	CE1	HIS	A	542	57.670	-9.669	47.055	1.00	15.74
3318	NE2	HIS	A	542	56.848	-8.690	46.754	1.00	14.08
3319	N	GLN	A	543	56.340	-7.489	53.425	1.00	19.61
3320	CA	GLN	A	543	55.955	-7.702	54.817	1.00	22.30
3321	C	GLN	A	543	54.786	-6.794	55.164	1.00	22.43
3322	O	GLN	A	543	54.023	-7.124	56.093	1.00	20.41
3323	CB	GLN	A	543	57.132	-7.462	55.797	1.00	23.32
3324	CG	GLN	A	543	58.247	-8.469	55.718	1.00	26.39
3325	CD	GLN	A	543	59.583	-8.082	56.334	1.00	29.94
3326	OE1	GLN	A	543	60.499	-8.911	56.516	1.00	29.73
3327	NE2	GLN	A	543	59.764	-6.816	56.705	1.00	28.77
3328	N	GLN	A	544	54.621	-5.649	54.503	1.00	21.34
3329	CA	GLN	A	544	53.444	-4.814	54.771	1.00	24.96
3330	C	GLN	A	544	52.339	-5.016	53.751	1.00	23.83
3331	O	GLN	A	544	51.495	-4.154	53.542	1.00	23.04
3332	CB	GLN	A	544	53.875	-3.348	54.782	1.00	29.05
3333	CG	GLN	A	544	54.974	-3.219	55.851	1.00	34.54
3334	CD	GLN	A	544	54.552	-3.697	57.224	1.00	37.02
3335	OE1	GLN	A	544	53.442	-3.372	57.648	1.00	39.96
3336	NE2	GLN	A	544	55.388	-4.465	57.921	1.00	38.54
3337	N	ARG	A	545	52.376	-6.121	53.023	1.00	24.22
3338	CA	ARG	A	545	51.393	-6.420	51.983	1.00	26.56
3339	C	ARG	A	545	51.405	-5.479	50.781	1.00	22.89
3340	O	ARG	A	545	50.354	-5.136	50.220	1.00	20.28
3341	CB	ARG	A	545	49.970	-6.500	52.565	1.00	32.05
3342	CG	ARG	A	545	49.843	-7.658	53.558	1.00	38.97
3343	CD	ARG	A	545	48.545	-8.386	53.314	1.00	45.28
3344	NE	ARG	A	545	47.466	-8.211	54.228	1.00	50.20
3345	CZ	ARG	A	545	46.728	-7.225	54.696	1.00	52.67
3346	NH1	ARG	A	545	46.938	-5.972	54.297	1.00	54.30
3347	NH2	ARG	A	545	45.760	-7.508	55.581	1.00	52.76
3348	N	ILE	A	546	52.568	-4.974	50.391	1.00	19.58
3349	CA	ILE	A	546	52.691	-4.154	49.197	1.00	18.16
3350	C	ILE	A	546	53.570	-4.849	48.165	1.00	17.48
3351	O	ILE	A	546	54.622	-5.411	48.473	1.00	13.86
3352	CB	ILE	A	546	53.198	-2.730	49.501	1.00	18.44
3353	CG1	ILE	A	546	52.267	-2.011	50.485	1.00	18.83
3354	CG2	ILE	A	546	53.319	-1.850	48.254	1.00	16.84
3355	CD1	ILE	A	546	52.910	-0.740	51.046	1.00	20.08
3356	N	GLY	A	547	53.077	-4.958	46.936	1.00	16.21
3357	CA	GLY	A	547	53.802	-5.583	45.845	1.00	13.51

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3358	C	GLY	A	547	54.760	-4.619	45.151	1.00	14.12
3359	O	GLY	A	547	54.720	-3.383	45.292	1.00	12.19
3360	N	VAL	A	548	55.614	-5.196	44.275	1.00	11.18
3361	CA	VAL	A	548	56.557	-4.349	43.534	1.00	11.75
3362	C	VAL	A	548	56.468	-4.674	42.042	1.00	12.64
3363	O	VAL	A	548	56.761	-5.829	41.654	1.00	11.98
3364	CB	VAL	A	548	57.995	-4.621	43.998	1.00	13.59
3365	CG1	VAL	A	548	58.998	-3.860	43.135	1.00	15.29
3366	CG2	VAL	A	548	58.278	-4.241	45.466	1.00	12.74
3367	N	ASN	A	549	56.225	-3.678	41.208	1.00	12.65
3368	CA	ASN	A	549	56.184	-3.878	39.757	1.00	13.79
3369	C	ASN	A	549	57.405	-3.147	39.191	1.00	15.40
3370	O	ASN	A	549	57.639	-1.977	39.536	1.00	14.02
3371	CB	ASN	A	549	54.882	-3.275	39.173	1.00	14.17
3372	CG	ASN	A	549	53.592	-4.005	39.512	1.00	15.52
3373	OD1	ASN	A	549	53.667	-5.127	40.037	1.00	15.71
3374	ND2	ASN	A	549	52.374	-3.530	39.214	1.00	11.04
3375	N	MET	A	550	58.240	-3.755	38.342	1.00	14.17
3376	CA	MET	A	550	59.397	-3.031	37.813	1.00	14.20
3377	C	MET	A	550	59.099	-2.392	36.448	1.00	14.75
3378	O	MET	A	550	58.661	-3.107	35.535	1.00	12.87
3379	CB	MET	A	550	60.626	-3.948	37.655	1.00	13.94
3380	CG	MET	A	550	61.452	-4.226	38.909	1.00	15.03
3381	SD	MET	A	550	62.697	-5.561	38.695	1.00	14.47
3382	CE	MET	A	550	63.764	-4.727	37.472	1.00	16.01
3383	N	ASP	A	551	59.368	-1.092	36.301	1.00	13.68
3384	CA	ASP	A	551	59.392	-0.396	35.011	1.00	14.18
3385	C	ASP	A	551	60.610	-0.949	34.274	1.00	15.34
3386	O	ASP	A	551	61.711	-0.908	34.871	1.00	16.12
3387	CB	ASP	A	551	59.565	1.119	35.255	1.00	13.46
3388	CG	ASP	A	551	59.452	1.990	34.034	1.00	14.83
3389	OD1	ASP	A	551	59.595	1.439	32.872	1.00	16.30
3390	OD2	ASP	A	551	59.255	3.209	34.103	1.00	12.40
3391	N	VAL	A	552	60.530	-1.561	33.107	1.00	15.18
3392	CA	VAL	A	552	61.659	-2.143	32.393	1.00	14.43
3393	C	VAL	A	552	61.698	-1.675	30.951	1.00	14.19
3394	O	VAL	A	552	60.693	-1.489	30.256	1.00	15.99
3395	CB	VAL	A	552	61.674	-3.691	32.386	1.00	14.09
3396	CG1	VAL	A	552	62.001	-4.194	33.795	1.00	11.24
3397	CG2	VAL	A	552	60.321	-4.237	31.901	1.00	11.60
3398	N	VAL	A	553	62.900	-1.482	30.427	1.00	13.93
3399	CA	VAL	A	553	63.153	-0.895	29.128	1.00	15.34
3400	C	VAL	A	553	63.848	-1.812	28.140	1.00	18.26
3401	O	VAL	A	553	64.912	-1.514	27.574	1.00	18.77
3402	CB	VAL	A	553	63.939	0.406	29.373	1.00	14.83
3403	CG1	VAL	A	553	64.111	1.249	28.108	1.00	17.28
3404	CG2	VAL	A	553	63.326	1.232	30.565	1.00	16.73
3405	N	TYR	A	554	63.251	-2.945	27.782	1.00	19.23
3406	CA	TYR	A	554	63.787	-3.864	26.789	1.00	17.41
3407	C	TYR	A	554	63.647	-3.343	25.367	1.00	17.63
3408	O	TYR	A	554	64.113	-4.065	24.465	1.00	18.06
3409	CB	TYR	A	554	63.080	-5.237	26.873	1.00	17.61
3410	CG	TYR	A	554	63.378	-5.873	28.232	1.00	16.57
3411	CD1	TYR	A	554	64.653	-6.384	28.473	1.00	17.67
3412	CD2	TYR	A	554	62.423	-5.941	29.222	1.00	16.40
3413	CE1	TYR	A	554	64.985	-6.939	29.706	1.00	17.79
3414	CE2	TYR	A	554	62.717	-6.544	30.457	1.00	17.52
3415	CZ	TYR	A	554	64.006	-7.002	30.692	1.00	17.50
3416	OH	TYR	A	554	64.325	-7.558	31.907	1.00	17.80
3417	N	ASN	A	555	62.967	-2.210	25.106	1.00	16.07
3418	CA	ASN	A	555	62.791	-1.817	23.708	1.00	15.21
3419	C	ASN	A	555	64.017	-1.220	23.038	1.00	15.49
3420	O	ASN	A	555	63.978	-1.070	21.805	1.00	16.91
3421	CB	ASN	A	555	61.570	-0.878	23.597	1.00	15.73
3422	CG	ASN	A	555	61.821	0.417	24.328	1.00	16.71
3423	OD1	ASN	A	555	62.555	1.260	23.818	1.00	16.20
3424	ND2	ASN	A	555	61.191	0.631	25.511	1.00	15.91
3425	N	HIS	A	556	65.054	-0.811	23.760	1.00	16.72
3426	CA	HIS	A	556	66.255	-0.226	23.128	1.00	18.73
3427	C	HIS	A	556	67.450	-0.203	24.091	1.00	18.92
3428	O	HIS	A	556	67.155	-0.343	25.279	1.00	20.30
3429	CB	HIS	A	556	65.917	1.214	22.682	1.00	17.52
3430	CG	HIS	A	556	65.912	2.220	23.794	1.00	18.40
3431	ND1	HIS	A	556	64.764	2.524	24.490	1.00	17.65
3432	CD2	HIS	A	556	66.886	2.964	24.365	1.00	18.54
3433	CE1	HIS	A	556	65.040	3.431	25.419	1.00	17.28
3434	NE2	HIS	A	556	66.303	3.717	25.383	1.00	17.13
3435	N	THR	A	557	68.719	-0.043	23.692	1.00	18.38
3436	CA	THR	A	557	69.798	0.042	24.644	1.00	18.28
3437	C	THR	A	557	70.323	1.476	24.705	1.00	17.57
3438	O	THR	A	557	69.911	2.301	23.856	1.00	14.70
3439	CB	THR	A	557	70.926	-0.963	24.352	1.00	19.68
3440	OG1	THR	A	557	71.497	-0.474	23.145	1.00	19.18
3441	CG2	THR	A	557	70.336	-2.357	24.042	1.00	18.93
3442	N	PHE	A	558	71.196	1.800	25.663	1.00	16.05
3443	CA	PHE	A	558	71.758	3.135	25.800	1.00	16.69
3444	C	PHE	A	558	72.400	3.664	24.505	1.00	18.93
3445	O	PHE	A	558	72.414	4.873	24.249	1.00	16.69
3446	CB	PHE	A	558	72.838	3.164	26.910	1.00	16.19
3447	CG	PHE	A	558	74.193	2.575	26.568	1.00	16.60
3448	CD1	PHE	A	558	74.357	1.190	26.467	1.00	16.91
3449	CD2	PHE	A	558	75.276	3.376	26.339	1.00	16.22
3450	CE1	PHE	A	558	75.602	0.649	26.161	1.00	19.59
3451	CE2	PHE	A	558	76.552	2.866	26.027	1.00	16.94
3452	CZ	PHE	A	558	76.715	1.484	25.941	1.00	18.98
3453	N	ASP	A	559	72.989	2.777	23.711	1.00	19.99

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3454	CA	ASP	A	559	73.645	3.165	22.465	1.00	24.77
3455	C	ASP	A	559	73.934	1.880	21.666	1.00	25.09
3456	O	ASP	A	559	73.574	0.768	22.077	1.00	24.21
3457	CB	ASP	A	559	74.907	3.979	22.708	1.00	26.93
3458	CG	ASP	A	559	75.484	4.649	21.466	1.00	31.80
3459	OD1	ASP	A	559	76.588	5.194	21.658	1.00	31.12
3460	OD2	ASP	A	559	74.883	4.689	20.357	1.00	31.41
3461	N	VAL	A	560	74.422	2.051	20.464	1.00	24.82
3462	CA	VAL	A	560	74.699	0.919	19.578	1.00	26.37
3463	C	VAL	A	560	76.162	0.933	19.226	1.00	26.33
3464	O	VAL	A	560	76.831	1.966	19.532	1.00	27.51
3465	CB	VAL	A	560	74.048	1.006	18.185	1.00	29.28
3466	CG1	VAL	A	560	72.537	0.936	18.394	1.00	31.23
3467	CG2	VAL	A	560	74.398	2.316	17.505	1.00	28.43
3468	N	MET	A	561	76.781	-0.011	18.554	1.00	26.30
3469	CA	MET	A	561	78.188	-0.013	18.178	1.00	26.74
3470	C	MET	A	561	79.185	-0.198	19.320	1.00	26.30
3471	O	MET	A	561	80.037	-1.085	19.319	1.00	24.56
3472	CB	MET	A	561	78.547	1.207	17.296	1.00	30.44
3473	CG	MET	A	561	77.954	0.954	15.881	1.00	34.34
3474	SD	MET	A	561	78.414	2.299	14.735	1.00	41.54
3475	CE	MET	A	561	77.950	3.727	15.746	1.00	37.55
3476	N	VAL	A	562	79.105	0.597	20.392	1.00	24.81
3477	CA	VAL	A	562	79.878	0.473	21.588	1.00	24.01
3478	C	VAL	A	562	79.185	-0.465	22.587	1.00	22.04
3479	O	VAL	A	562	79.767	-0.601	23.647	1.00	22.34
3480	CB	VAL	A	562	80.058	1.821	22.350	1.00	24.42
3481	CG1	VAL	A	562	80.934	2.745	21.496	1.00	24.85
3482	CG2	VAL	A	562	78.780	2.479	22.759	1.00	21.36
3483	N	SER	A	563	78.011	-1.007	22.251	1.00	20.50
3484	CA	SER	A	563	77.297	-1.820	23.238	1.00	20.03
3485	C	SER	A	563	77.836	-3.239	23.199	1.00	17.42
3486	O	SER	A	563	78.348	-3.629	22.143	1.00	17.90
3487	CB	SER	A	563	75.773	-1.854	23.035	1.00	20.21
3488	OG	SER	A	563	75.504	-2.439	21.727	1.00	19.79
3489	N	ASP	A	564	77.647	-3.985	24.276	1.00	15.82
3490	CA	ASP	A	564	78.065	-5.390	24.327	1.00	15.51
3491	C	ASP	A	564	77.410	-6.216	23.241	1.00	16.59
3492	O	ASP	A	564	78.055	-7.027	22.529	1.00	15.21
3493	CB	ASP	A	564	77.720	-5.977	25.726	1.00	16.55
3494	CG	ASP	A	564	78.581	-5.296	26.800	1.00	18.34
3495	OD1	ASP	A	564	79.821	-5.219	26.651	1.00	17.26
3496	OD2	ASP	A	564	78.037	-4.798	27.810	1.00	17.62
3497	N	PHE	A	565	76.111	-5.973	23.019	1.00	13.96
3498	CA	PHE	A	565	75.399	-6.655	21.943	1.00	15.67
3499	C	PHE	A	565	76.139	-6.483	20.599	1.00	14.63
3500	O	PHE	A	565	76.355	-7.509	19.924	1.00	13.99
3501	CB	PHE	A	565	73.912	-6.291	21.789	1.00	16.58
3502	CG	PHE	A	565	72.997	-6.694	22.894	1.00	20.85
3503	CD1	PHE	A	565	72.139	-5.782	23.477	1.00	26.06
3504	CD2	PHE	A	565	72.967	-7.987	23.380	1.00	23.43
3505	CE1	PHE	A	565	71.283	-6.128	24.537	1.00	28.11
3506	CE2	PHE	A	565	72.117	-8.352	24.417	1.00	24.43
3507	CZ	PHE	A	565	71.293	-7.438	25.000	1.00	25.83
3508	N	ASP	A	566	76.440	-5.285	20.148	1.00	14.36
3509	CA	ASP	A	566	77.110	-5.056	18.855	1.00	15.72
3510	C	ASP	A	566	78.563	-5.512	18.779	1.00	17.43
3511	O	ASP	A	566	79.047	-5.871	17.691	1.00	19.46
3512	CB	ASP	A	566	77.041	-3.554	18.495	1.00	15.76
3513	CG	ASP	A	566	75.837	-3.207	17.621	1.00	18.28
3514	OD1	ASP	A	566	75.121	-4.134	17.172	1.00	17.60
3515	OD2	ASP	A	566	75.529	-1.986	17.464	1.00	18.93
3516	N	LYS	A	567	79.280	-5.618	19.905	1.00	16.44
3517	CA	LYS	A	567	80.648	-6.126	19.938	1.00	17.53
3518	C	LYS	A	567	80.694	-7.648	19.878	1.00	17.64
3519	O	LYS	A	567	81.712	-8.259	19.540	1.00	17.11
3520	CB	LYS	A	567	81.414	-5.609	21.194	1.00	17.62
3521	CG	LYS	A	567	81.622	-4.074	21.089	1.00	18.85
3522	CD	LYS	A	567	82.538	-3.543	22.204	1.00	18.13
3523	CE	LYS	A	567	81.848	-3.502	23.564	1.00	18.33
3524	NZ	LYS	A	567	82.816	-3.195	24.678	1.00	16.66
3525	N	ILE	A	568	79.612	-8.349	20.201	1.00	16.25
3526	CA	ILE	A	568	79.549	-9.800	20.123	1.00	16.20
3527	C	ILE	A	568	78.908	-10.273	18.823	1.00	17.07
3528	O	ILE	A	568	79.382	-11.238	18.178	1.00	14.48
3529	CB	ILE	A	568	78.818	-10.362	21.376	1.00	16.15
3530	CG1	ILE	A	568	79.514	-9.915	22.665	1.00	15.42
3531	CG2	ILE	A	568	78.774	-11.890	21.304	1.00	14.58
3532	CD1	ILE	A	568	78.696	-10.199	23.951	1.00	17.78
3533	N	VAL	A	569	77.730	-9.732	18.434	1.00	15.69
3534	CA	VAL	A	569	77.048	-10.133	17.196	1.00	15.88
3535	C	VAL	A	569	76.626	-8.839	16.471	1.00	16.98
3536	O	VAL	A	569	75.525	-8.306	16.695	1.00	15.04
3537	CB	VAL	A	569	75.807	-11.021	17.396	1.00	15.85
3538	CG1	VAL	A	569	75.416	-11.682	16.074	1.00	14.38
3539	CG2	VAL	A	569	75.972	-12.073	18.504	1.00	14.02
3540	N	PRO	A	570	77.515	-8.315	15.624	1.00	15.25
3541	CA	PRO	A	570	77.309	-7.021	14.982	1.00	16.13
3542	C	PRO	A	570	75.950	-6.794	14.359	1.00	16.17
3543	O	PRO	A	570	75.466	-7.600	13.555	1.00	15.22
3544	CB	PRO	A	570	78.472	-6.901	14.010	1.00	17.25
3545	CG	PRO	A	570	79.570	-7.724	14.640	1.00	16.61
3546	CD	PRO	A	570	78.844	-8.878	15.311	1.00	15.81
3547	N	GLN	A	571	75.257	-5.746	14.775	1.00	14.50
3548	CA	GLN	A	571	73.918	-5.303	14.447	1.00	14.80
3549	C	GLN	A	571	72.705	-6.160	14.739	1.00	16.27

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3550	O	GLN	A	571	71.549	-5.639	14.722	1.00	13.56
3551	CB	GLN	A	571	73.748	-4.892	12.953	1.00	15.26
3552	CG	GLN	A	571	74.766	-3.823	12.497	1.00	15.43
3553	CD	GLN	A	571	74.503	-3.354	11.059	1.00	19.19
3554	OE1	GLN	A	571	73.563	-3.777	10.388	1.00	18.40
3555	NE2	GLN	A	571	75.367	-2.510	10.508	1.00	16.57
3556	N	TYR	A	572	72.855	-7.469	14.886	1.00	16.66
3557	CA	TYR	A	572	71.762	-8.426	14.967	1.00	16.46
3558	C	TYR	A	572	70.762	-8.214	16.097	1.00	15.79
3559	O	TYR	A	572	69.571	-8.534	15.888	1.00	15.97
3560	CB	TYR	A	572	72.356	-9.851	15.074	1.00	15.56
3561	CG	TYR	A	572	71.265	-10.918	14.864	1.00	16.45
3562	CD1	TYR	A	572	70.668	-11.104	13.618	1.00	15.36
3563	CD2	TYR	A	572	70.776	-11.624	15.938	1.00	15.32
3564	CE1	TYR	A	572	69.678	-12.067	13.462	1.00	16.37
3565	CE2	TYR	A	572	69.793	-12.590	15.799	1.00	16.69
3566	CZ	TYR	A	572	69.237	-12.809	14.543	1.00	16.67
3567	OH	TYR	A	572	68.200	-13.718	14.410	1.00	15.39
3568	N	TYR	A	573	71.134	-7.671	17.246	1.00	16.43
3569	CA	TYR	A	573	70.136	-7.459	18.322	1.00	17.97
3570	C	TYR	A	573	69.259	-6.225	18.096	1.00	17.17
3571	O	TYR	A	573	68.347	-5.946	18.884	1.00	13.58
3572	CB	TYR	A	573	70.852	-7.342	19.679	1.00	18.07
3573	CG	TYR	A	573	71.414	-8.647	20.227	1.00	20.16
3574	CD1	TYR	A	573	72.722	-9.044	20.012	1.00	19.58
3575	CD2	TYR	A	573	70.603	-9.487	21.008	1.00	20.25
3576	CE1	TYR	A	573	73.204	-10.247	20.549	1.00	20.41
3577	CE2	TYR	A	573	71.064	-10.682	21.552	1.00	19.87
3578	CZ	TYR	A	573	72.388	-11.041	21.317	1.00	20.91
3579	OH	TYR	A	573	72.862	-12.222	21.864	1.00	20.44
3580	N	TYR	A	574	69.515	-5.474	17.014	1.00	16.82
3581	CA	TYR	A	574	68.727	-4.275	16.718	1.00	15.66
3582	C	TYR	A	574	68.004	-4.350	15.382	1.00	16.73
3583	O	TYR	A	574	68.406	-5.134	14.504	1.00	18.00
3584	CB	TYR	A	574	69.665	-3.067	16.759	1.00	15.38
3585	CG	TYR	A	574	70.493	-2.931	18.020	1.00	18.02
3586	CD1	TYR	A	574	69.924	-2.327	19.156	1.00	17.70
3587	CD2	TYR	A	574	71.787	-3.466	18.124	1.00	18.97
3588	CE1	TYR	A	574	70.640	-2.205	20.327	1.00	16.27
3589	CE2	TYR	A	574	72.507	-3.336	19.319	1.00	18.59
3590	CZ	TYR	A	574	71.932	-2.685	20.399	1.00	18.97
3591	OH	TYR	A	574	72.633	-2.523	21.588	1.00	18.86
3592	N	ARG	A	575	66.949	-3.552	15.167	1.00	14.99
3593	CA	ARG	A	575	66.271	-3.493	13.869	1.00	15.92
3594	C	ARG	A	575	66.986	-2.557	12.896	1.00	16.49
3595	O	ARG	A	575	67.443	-1.428	13.268	1.00	14.85
3596	CB	ARG	A	575	64.798	-3.050	14.073	1.00	15.06
3597	CG	ARG	A	575	63.996	-3.916	15.070	1.00	15.86
3598	CD	ARG	A	575	62.468	-3.788	14.882	1.00	16.88
3599	NE	ARG	A	575	61.750	-4.691	15.785	1.00	13.65
3600	CZ	ARG	A	575	61.087	-4.506	16.914	1.00	16.15
3601	NH1	ARG	A	575	60.840	-3.302	17.495	1.00	13.01
3602	NH2	ARG	A	575	60.591	-5.606	17.516	1.00	11.72
3603	N	THR	A	576	67.240	-3.018	11.669	1.00	17.48
3604	CA	THR	A	576	67.911	-2.206	10.648	1.00	16.92
3605	C	THR	A	576	67.062	-2.149	9.365	1.00	18.54
3606	O	THR	A	576	66.283	-3.087	9.134	1.00	19.15
3607	CB	THR	A	576	69.304	-2.708	10.228	1.00	17.51
3608	OG1	THR	A	576	69.224	-4.053	9.768	1.00	12.75
3609	CG2	THR	A	576	70.351	-2.561	11.345	1.00	18.13
3610	N	ASP	A	577	67.206	-1.088	8.567	1.00	18.10
3611	CA	ASP	A	577	66.406	-0.999	7.351	1.00	18.80
3612	C	ASP	A	577	67.218	-1.512	6.154	1.00	20.47
3613	O	ASP	A	577	68.348	-2.037	6.306	1.00	22.66
3614	CB	ASP	A	577	65.858	0.404	7.051	1.00	18.16
3615	CG	ASP	A	577	66.941	1.424	6.856	1.00	19.10
3616	OD1	ASP	A	577	66.636	2.634	7.169	1.00	19.08
3617	OD2	ASP	A	577	68.119	1.198	6.485	1.00	16.70
3618	N	SER	A	578	66.674	-1.364	4.963	1.00	20.77
3619	CA	SER	A	578	67.276	-1.837	3.705	1.00	21.43
3620	C	SER	A	578	68.503	-1.061	3.308	1.00	21.24
3621	O	SER	A	578	69.334	-1.575	2.544	1.00	21.58
3622	CB	SER	A	578	66.212	-1.815	2.599	1.00	23.81
3623	OG	SER	A	578	65.419	-2.993	2.665	1.00	24.09
3624	N	ASN	A	579	68.692	0.150	3.800	1.00	21.04
3625	CA	ASN	A	579	69.893	0.918	3.551	1.00	22.84
3626	C	ASN	A	579	71.069	0.581	4.470	1.00	22.28
3627	O	ASN	A	579	72.244	1.070	4.370	1.00	22.77
3628	CB	ASN	A	579	69.572	2.403	3.670	1.00	24.77
3629	CG	ASN	A	579	68.611	2.929	2.641	1.00	27.96
3630	OD1	ASN	A	579	67.940	3.947	2.900	1.00	30.34
3631	ND2	ASN	A	579	68.431	2.198	1.548	1.00	27.67
3632	N	GLY	A	580	70.811	-0.191	5.501	1.00	21.69
3633	CA	GLY	A	580	71.749	-0.563	6.551	1.00	20.67
3634	C	GLY	A	580	71.708	0.335	7.781	1.00	20.28
3635	O	GLY	A	580	72.723	0.373	8.505	1.00	20.34
3636	N	ASN	A	581	70.727	1.230	7.907	1.00	19.77
3637	CA	ASN	A	581	70.647	2.096	9.057	1.00	20.14
3638	C	ASN	A	581	69.811	1.448	10.186	1.00	20.05
3639	O	ASN	A	581	68.809	0.802	9.843	1.00	20.06
3640	CB	ASN	A	581	70.061	3.486	8.758	1.00	20.77
3641	CG	ASN	A	581	70.979	4.271	7.815	1.00	24.55
3642	OD1	ASN	A	581	72.201	4.336	7.991	1.00	25.71
3643	ND2	ASN	A	581	70.436	4.847	6.760	1.00	22.88
3644	N	TYR	A	582	70.211	1.744	11.428	1.00	18.90
3645	CA	TYR	A	582	69.377	1.345	12.592	1.00	20.45

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3646	C	TYR	A	582	68.045	2.071	12.591	1.00	18.67
3647	O	TYR	A	582	68.050	3.319	12.396	1.00	17.45
3648	CB	TYR	A	582	70.093	1.730	13.900	1.00	21.60
3649	CG	TYR	A	582	71.394	0.997	14.143	1.00	26.25
3650	CD1	TYR	A	582	72.639	1.501	13.726	1.00	27.97
3651	CD2	TYR	A	582	71.374	-0.230	14.777	1.00	27.31
3652	CE1	TYR	A	582	73.853	0.831	13.960	1.00	28.48
3653	CE2	TYR	A	582	72.561	-0.924	15.000	1.00	28.99
3654	CZ	TYR	A	582	73.774	-0.390	14.589	1.00	28.99
3655	OH	TYR	A	582	74.899	-1.115	14.864	1.00	28.24
3656	N	THR	A	583	66.912	1.437	12.737	1.00	18.57
3657	CA	THR	A	583	65.623	2.143	12.764	1.00	19.17
3658	C	THR	A	583	65.399	2.672	14.204	1.00	19.21
3659	O	THR	A	583	66.002	2.240	15.227	1.00	15.73
3660	CB	THR	A	583	64.442	1.271	12.295	1.00	21.01
3661	OG1	THR	A	583	64.334	0.091	13.179	1.00	19.15
3662	CG2	THR	A	583	64.598	0.758	10.847	1.00	20.19
3663	N	ASN	A	584	64.574	3.728	14.303	1.00	16.30
3664	CA	ASN	A	584	64.420	4.507	15.514	1.00	17.48
3665	C	ASN	A	584	63.063	4.434	16.164	1.00	17.05
3666	O	ASN	A	584	62.469	5.447	16.559	1.00	16.19
3667	CB	ASN	A	584	64.779	5.966	15.133	1.00	19.28
3668	CG	ASN	A	584	65.141	6.823	16.319	1.00	20.58
3669	OD1	ASN	A	584	65.304	6.339	17.435	1.00	22.86
3670	ND2	ASN	A	584	65.101	8.148	16.199	1.00	22.27
3671	N	GLY	A	585	62.499	3.249	16.338	1.00	17.36
3672	CA	GLY	A	585	61.169	3.095	16.940	1.00	18.20
3673	C	GLY	A	585	61.073	3.688	18.348	1.00	19.43
3674	O	GLY	A	585	60.000	4.151	18.739	1.00	17.42
3675	N	SER	A	586	62.149	3.685	19.128	1.00	20.93
3676	CA	SER	A	586	62.095	4.195	20.490	1.00	21.54
3677	C	SER	A	586	62.259	5.711	20.590	1.00	20.81
3678	O	SER	A	586	61.993	6.277	21.652	1.00	20.13
3679	CB	SER	A	586	63.221	3.538	21.302	1.00	20.63
3680	OG	SER	A	586	64.491	4.039	20.840	1.00	21.23
3681	N	GLY	A	587	62.771	6.354	19.558	1.00	19.63
3682	CA	GLY	A	587	63.102	7.781	19.629	1.00	20.56
3683	C	GLY	A	587	64.469	8.006	20.279	1.00	21.87
3684	O	GLY	A	587	64.930	9.158	20.346	1.00	21.43
3685	N	CYS	A	588	65.213	6.945	20.630	1.00	19.06
3686	CA	CYS	A	588	66.495	7.043	21.300	1.00	19.09
3687	C	CYS	A	588	67.651	6.569	20.417	1.00	20.16
3688	O	CYS	A	588	68.797	6.442	20.864	1.00	18.88
3689	CB	CYS	A	588	66.462	6.167	22.569	1.00	18.06
3690	SG	CYS	A	588	65.249	6.772	23.792	1.00	20.94
3691	N	GLY	A	589	67.358	6.343	19.130	1.00	19.74
3692	CA	GLY	A	589	68.464	5.999	18.224	1.00	20.77
3693	C	GLY	A	589	68.511	4.521	17.843	1.00	20.75
3694	O	GLY	A	589	69.319	4.222	16.957	1.00	21.38
3695	N	ASN	A	590	67.768	3.611	18.454	1.00	18.78
3696	CA	ASN	A	590	67.823	2.183	18.077	1.00	17.60
3697	C	ASN	A	590	66.576	1.529	18.652	1.00	17.96
3698	O	ASN	A	590	65.865	2.190	19.463	1.00	17.56
3699	CB	ASN	A	590	69.087	1.484	18.624	1.00	15.88
3700	CG	ASN	A	590	69.144	1.355	20.139	1.00	17.35
3701	OD1	ASN	A	590	68.469	0.536	20.774	1.00	15.30
3702	ND2	ASN	A	590	69.897	2.207	20.808	1.00	15.71
3703	N	GLU	A	591	66.335	0.275	18.302	1.00	17.77
3704	CA	GLU	A	591	65.200	-0.435	18.873	1.00	18.01
3705	C	GLU	A	591	65.575	-1.923	18.828	1.00	18.01
3706	O	GLU	A	591	66.264	-2.419	17.909	1.00	17.69
3707	CB	GLU	A	591	63.831	-0.072	18.251	1.00	19.26
3708	CG	GLU	A	591	63.658	-0.382	16.805	1.00	18.33
3709	CD	GLU	A	591	62.322	-0.090	16.134	1.00	19.76
3710	OE1	GLU	A	591	62.383	0.617	15.092	1.00	18.91
3711	OE2	GLU	A	591	61.249	-0.589	16.551	1.00	18.36
3712	N	PHE	A	592	65.262	-2.635	19.900	1.00	15.35
3713	CA	PHE	A	592	65.646	-4.041	20.070	1.00	18.51
3714	C	PHE	A	592	64.787	-4.958	19.219	1.00	16.58
3715	O	PHE	A	592	63.532	-4.916	19.203	1.00	18.31
3716	CB	PHE	A	592	65.507	-4.390	21.572	1.00	18.66
3717	CG	PHE	A	592	66.320	-5.575	22.007	1.00	19.55
3718	CD1	PHE	A	592	67.687	-5.484	22.227	1.00	21.67
3719	CD2	PHE	A	592	65.700	-6.800	22.204	1.00	21.14
3720	CE1	PHE	A	592	68.400	-6.593	22.666	1.00	21.13
3721	CE2	PHE	A	592	66.399	-7.894	22.657	1.00	21.68
3722	CZ	PHE	A	592	67.750	-7.786	22.877	1.00	20.22
3723	N	ALA	A	593	65.422	-5.805	18.433	1.00	15.23
3724	CA	ALA	A	593	64.731	-6.643	17.459	1.00	14.58
3725	C	ALA	A	593	64.218	-7.941	18.052	1.00	15.78
3726	O	ALA	A	593	64.818	-8.986	17.839	1.00	15.37
3727	CB	ALA	A	593	65.653	-6.921	16.263	1.00	14.49
3728	N	THR	A	594	63.084	-7.909	18.737	1.00	13.64
3729	CA	THR	A	594	62.430	-9.049	19.319	1.00	17.21
3730	C	THR	A	594	61.898	-10.007	18.255	1.00	18.41
3731	O	THR	A	594	61.673	-11.162	18.635	1.00	16.76
3732	CB	THR	A	594	61.234	-8.677	20.250	1.00	15.31
3733	OG1	THR	A	594	60.306	-7.885	19.481	1.00	16.09
3734	CG2	THR	A	594	61.715	-7.890	21.453	1.00	15.49
3735	N	GLU	A	595	61.862	-9.680	16.956	1.00	17.58
3736	CA	GLU	A	595	61.519	-10.670	15.952	1.00	17.42
3737	C	GLU	A	595	62.715	-11.589	15.648	1.00	18.14
3738	O	GLU	A	595	62.627	-12.532	14.859	1.00	19.18
3739	CB	GLU	A	595	60.966	-10.097	14.646	1.00	18.92
3740	CG	GLU	A	595	61.955	-9.284	13.797	1.00	17.41
3741	CD	GLU	A	595	62.217	-7.889	14.333	1.00	18.02

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3742	OE1	GLU	A	595	61.964	-7.461	15.493	1.00	16.28
3743	OE2	GLU	A	595	62.768	-7.075	13.557	1.00	18.81
3744	N	HIS	A	596	63.900	-11.351	16.189	1.00	16.45
3745	CA	HIS	A	596	65.050	-12.239	15.996	1.00	15.59
3746	C	HIS	A	596	65.076	-13.182	17.190	1.00	16.08
3747	O	HIS	A	596	65.031	-12.701	18.324	1.00	15.72
3748	CB	HIS	A	596	66.324	-11.404	15.934	1.00	14.25
3749	CG	HIS	A	596	66.598	-10.769	14.592	1.00	16.18
3750	ND1	HIS	A	596	67.579	-9.788	14.434	1.00	14.53
3751	CD2	HIS	A	596	66.014	-10.918	13.388	1.00	13.81
3752	CE1	HIS	A	596	67.617	-9.420	13.163	1.00	15.09
3753	NE2	HIS	A	596	66.708	-10.116	12.524	1.00	15.29
3754	N	PRO	A	597	64.965	-14.485	16.976	1.00	16.49
3755	CA	PRO	A	597	64.763	-15.436	18.023	1.00	17.55
3756	C	PRO	A	597	65.654	-15.307	19.250	1.00	18.38
3757	O	PRO	A	597	65.097	-15.446	20.358	1.00	17.58
3758	CB	PRO	A	597	64.928	-16.799	17.319	1.00	17.50
3759	CG	PRO	A	597	64.306	-16.514	15.953	1.00	18.51
3760	CD	PRO	A	597	64.817	-15.129	15.637	1.00	18.53
3761	N	MET	A	598	66.964	-15.173	19.087	1.00	15.98
3762	CA	MET	A	598	67.874	-15.133	20.231	1.00	15.82
3763	C	MET	A	598	67.729	-13.791	20.940	1.00	15.34
3764	O	MET	A	598	68.082	-13.708	22.130	1.00	16.95
3765	CB	MET	A	598	69.336	-15.412	19.803	1.00	16.00
3766	CG	MET	A	598	69.574	-16.841	19.325	1.00	13.68
3767	SD	MET	A	598	69.207	-18.085	20.579	1.00	13.98
3768	CE	MET	A	598	70.593	-17.828	21.697	1.00	15.11
3769	N	ALA	A	599	67.344	-12.740	20.202	1.00	14.72
3770	CA	ALA	A	599	67.059	-11.481	20.876	1.00	15.20
3771	C	ALA	A	599	65.783	-11.665	21.708	1.00	16.47
3772	O	ALA	A	599	65.749	-11.281	22.874	1.00	17.10
3773	CB	ALA	A	599	66.943	-10.328	19.898	1.00	13.55
3774	N	GLN	A	600	64.731	-12.308	21.178	1.00	16.72
3775	CA	GLN	A	600	63.525	-12.575	21.946	1.00	18.51
3776	C	GLN	A	600	63.860	-13.406	23.201	1.00	17.76
3777	O	GLN	A	600	63.429	-13.048	24.311	1.00	13.69
3778	CB	GLN	A	600	62.404	-13.240	21.137	1.00	17.71
3779	CG	GLN	A	600	61.117	-13.534	21.935	1.00	16.56
3780	CD	GLN	A	600	60.174	-14.357	21.052	1.00	16.99
3781	OE1	GLN	A	600	60.365	-15.573	20.886	1.00	17.99
3782	NE2	GLN	A	600	59.183	-13.690	20.475	1.00	12.76
3783	N	LYS	A	601	64.723	-14.418	23.042	1.00	17.63
3784	CA	LYS	A	601	65.138	-15.279	24.130	1.00	17.70
3785	C	LYS	A	601	65.881	-14.491	25.221	1.00	18.25
3786	O	LYS	A	601	65.662	-14.783	26.399	1.00	16.32
3787	CB	LYS	A	601	66.023	-16.457	23.633	1.00	18.32
3788	CG	LYS	A	601	66.619	-17.286	24.778	1.00	17.88
3789	CD	LYS	A	601	67.393	-18.512	24.279	1.00	18.60
3790	CE	LYS	A	601	68.237	-19.167	25.397	1.00	18.85
3791	NZ	LYS	A	601	67.398	-19.618	26.571	1.00	16.70
3792	N	PHE	A	602	66.732	-13.517	24.854	1.00	17.63
3793	CA	PHE	A	602	67.370	-12.649	25.854	1.00	16.13
3794	C	PHE	A	602	66.329	-12.012	26.764	1.00	16.27
3795	O	PHE	A	602	66.554	-11.907	28.009	1.00	14.81
3796	CB	PHE	A	602	68.204	-11.538	25.161	1.00	16.06
3797	CG	PHE	A	602	68.846	-10.590	26.149	1.00	16.65
3798	CD1	PHE	A	602	68.244	-9.406	26.531	1.00	15.22
3799	CD2	PHE	A	602	70.050	-10.983	26.751	1.00	17.45
3800	CE1	PHE	A	602	68.808	-8.625	27.539	1.00	16.75
3801	CE2	PHE	A	602	70.620	-10.201	27.747	1.00	17.98
3802	CZ	PHE	A	602	70.006	-9.011	28.135	1.00	15.11
3803	N	VAL	A	603	65.258	-11.426	26.171	1.00	15.45
3804	CA	VAL	A	603	64.237	-10.777	27.017	1.00	15.99
3805	C	VAL	A	603	63.494	-11.778	27.884	1.00	16.06
3806	O	VAL	A	603	63.312	-11.545	29.095	1.00	16.02
3807	CB	VAL	A	603	63.212	-9.946	26.186	1.00	18.42
3808	CG1	VAL	A	603	62.219	-9.197	27.073	1.00	14.68
3809	CG2	VAL	A	603	63.961	-8.957	25.276	1.00	15.72
3810	N	LEU	A	604	63.039	-12.897	27.353	1.00	13.96
3811	CA	LEU	A	604	62.322	-13.923	28.086	1.00	15.23
3812	C	LEU	A	604	63.112	-14.470	29.269	1.00	17.26
3813	O	LEU	A	604	62.593	-14.609	30.374	1.00	14.68
3814	CB	LEU	A	604	61.903	-15.076	27.150	1.00	18.02
3815	CG	LEU	A	604	60.794	-14.774	26.119	1.00	19.15
3816	CD1	LEU	A	604	60.645	-15.892	25.085	1.00	19.70
3817	CD2	LEU	A	604	59.464	-14.593	26.844	1.00	21.10
3818	N	ASP	A	605	64.415	-14.727	29.072	1.00	15.26
3819	CA	ASP	A	605	65.315	-15.216	30.095	1.00	16.47
3820	C	ASP	A	605	65.424	-14.164	31.216	1.00	16.78
3821	O	ASP	A	605	65.426	-14.517	32.390	1.00	15.91
3822	CB	ASP	A	605	66.722	-15.477	29.523	1.00	14.57
3823	CG	ASP	A	605	66.881	-16.749	28.698	1.00	18.15
3824	OD1	ASP	A	605	67.938	-16.953	28.012	1.00	14.80
3825	OD2	ASP	A	605	65.927	-17.564	28.720	1.00	15.40
3826	N	SER	A	606	65.555	-12.903	30.809	1.00	15.59
3827	CA	SER	A	606	65.716	-11.772	31.721	1.00	14.83
3828	C	SER	A	606	64.501	-11.560	32.614	1.00	14.39
3829	O	SER	A	606	64.675	-11.460	33.840	1.00	13.45
3830	CB	SER	A	606	66.094	-10.483	30.977	1.00	14.58
3831	OG	SER	A	606	66.281	-9.390	31.898	1.00	14.28
3832	N	VAL	A	607	63.265	-11.480	32.095	1.00	14.64
3833	CA	VAL	A	607	62.127	-11.281	33.004	1.00	15.38
3834	C	VAL	A	607	61.945	-12.521	33.896	1.00	15.96
3835	O	VAL	A	607	61.514	-12.318	35.035	1.00	15.28
3836	CB	VAL	A	607	60.810	-10.937	32.280	1.00	15.47
3837	CG1	VAL	A	607	60.974	-9.551	31.618	1.00	13.07

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3838	CG2	VAL	A	607	60.425	-12.035	31.284	1.00	12.85
3839	N	ASN	A	608	62.193	-13.746	33.446	1.00	14.92
3840	CA	ASN	A	608	62.161	-14.916	34.299	1.00	16.74
3841	C	ASN	A	608	63.201	-14.835	35.444	1.00	17.85
3842	O	ASN	A	608	62.877	-15.128	36.608	1.00	17.58
3843	CB	ASN	A	608	62.493	-16.209	33.518	1.00	19.59
3844	CG	ASN	A	608	61.296	-16.876	32.872	1.00	22.08
3845	OD1	ASN	A	608	60.979	-16.711	31.678	1.00	25.08
3846	ND2	ASN	A	608	60.495	-17.611	33.626	1.00	20.95
3847	N	TYR	A	609	64.415	-14.328	35.175	1.00	15.99
3848	CA	TYR	A	609	65.427	-14.137	36.228	1.00	15.94
3849	C	TYR	A	609	64.972	-13.130	37.284	1.00	17.05
3850	O	TYR	A	609	65.128	-13.371	38.504	1.00	15.91
3851	CB	TYR	A	609	66.775	-13.708	35.575	1.00	15.56
3852	CG	TYR	A	609	67.853	-13.313	36.573	1.00	16.22
3853	CD1	TYR	A	609	68.489	-14.266	37.390	1.00	16.45
3854	CD2	TYR	A	609	68.197	-12.002	36.736	1.00	16.36
3855	CE1	TYR	A	609	69.470	-13.877	38.289	1.00	17.53
3856	CE2	TYR	A	609	69.169	-11.603	37.661	1.00	17.03
3857	CZ	TYR	A	609	69.731	-12.544	38.487	1.00	17.07
3858	OH	TYR	A	609	70.710	-12.140	39.389	1.00	18.77
3859	N	TRP	A	610	64.391	-11.975	36.873	1.00	15.33
3860	CA	TRP	A	610	63.997	-10.954	37.843	1.00	14.87
3861	C	TRP	A	610	62.906	-11.516	38.749	1.00	17.00
3862	O	TRP	A	610	62.946	-11.295	39.934	1.00	15.43
3863	CB	TRP	A	610	63.571	-9.617	37.205	1.00	16.60
3864	CG	TRP	A	610	64.795	-8.841	36.758	1.00	17.32
3865	CD1	TRP	A	610	65.385	-8.826	35.530	1.00	18.14
3866	CD2	TRP	A	610	65.604	-8.000	37.606	1.00	16.87
3867	NE1	TRP	A	610	66.501	-8.032	35.528	1.00	17.52
3868	CE2	TRP	A	610	66.670	-7.524	36.816	1.00	17.86
3869	CE3	TRP	A	610	65.507	-7.619	38.949	1.00	16.40
3870	CZ2	TRP	A	610	67.624	-6.629	37.310	1.00	17.05
3871	CZ3	TRP	A	610	66.480	-6.768	39.473	1.00	18.04
3872	CH2	TRP	A	610	67.519	-6.256	38.646	1.00	16.76
3873	N	VAL	A	611	61.917	-12.259	38.217	1.00	17.68
3874	CA	VAL	A	611	60.891	-12.872	39.051	1.00	17.19
3875	C	VAL	A	611	61.481	-13.944	39.976	1.00	17.50
3876	O	VAL	A	611	61.150	-13.951	41.159	1.00	17.52
3877	CB	VAL	A	611	59.784	-13.473	38.166	1.00	16.45
3878	CG1	VAL	A	611	58.825	-14.397	38.941	1.00	13.42
3879	CG2	VAL	A	611	58.959	-12.335	37.537	1.00	15.16
3880	N	ASN	A	612	62.221	-14.917	39.491	1.00	17.95
3881	CA	ASN	A	612	62.770	-15.986	40.314	1.00	19.97
3882	C	ASN	A	612	63.769	-15.479	41.361	1.00	20.64
3883	O	ASN	A	612	63.629	-15.773	42.566	1.00	19.49
3884	CB	ASN	A	612	63.350	-17.062	39.398	1.00	23.07
3885	CG	ASN	A	612	62.330	-17.925	38.661	1.00	27.67
3886	OD1	ASN	A	612	62.706	-18.413	37.561	1.00	30.76
3887	ND2	ASN	A	612	61.091	-18.211	39.114	1.00	23.39
3888	N	GLU	A	613	64.794	-14.722	40.987	1.00	17.75
3889	CA	GLU	A	613	65.784	-14.237	41.933	1.00	16.91
3890	C	GLU	A	613	65.325	-13.120	42.851	1.00	16.20
3891	O	GLU	A	613	65.810	-13.011	44.017	1.00	15.78
3892	CB	GLU	A	613	67.044	-13.805	41.121	1.00	17.72
3893	CG	GLU	A	613	68.292	-13.483	41.942	1.00	17.78
3894	CD	GLU	A	613	68.895	-14.683	42.660	1.00	19.51
3895	OE1	GLU	A	613	68.818	-15.820	42.180	1.00	18.15
3896	OE2	GLU	A	613	69.413	-14.521	43.782	1.00	21.38
3897	N	TYR	A	614	64.583	-12.123	42.358	1.00	14.53
3898	CA	TYR	A	614	64.252	-10.958	43.180	1.00	14.18
3899	C	TYR	A	614	62.805	-11.002	43.696	1.00	17.41
3900	O	TYR	A	614	62.446	-10.102	44.461	1.00	17.30
3901	CB	TYR	A	614	64.553	-9.677	42.390	1.00	13.30
3902	CG	TYR	A	614	66.058	-9.370	42.201	1.00	14.37
3903	CD1	TYR	A	614	66.759	-8.589	43.088	1.00	14.58
3904	CD2	TYR	A	614	66.753	-9.907	41.128	1.00	13.92
3905	CE1	TYR	A	614	68.139	-8.317	42.936	1.00	14.22
3906	CE2	TYR	A	614	68.120	-9.659	40.942	1.00	13.85
3907	CZ	TYR	A	614	68.795	-8.864	41.857	1.00	15.00
3908	OH	TYR	A	614	70.152	-8.611	41.699	1.00	13.86
3909	N	HIS	A	615	61.982	-11.968	43.309	1.00	16.00
3910	CA	HIS	A	615	60.589	-12.094	43.716	1.00	18.34
3911	C	HIS	A	615	59.671	-10.919	43.363	1.00	18.85
3912	O	HIS	A	615	58.762	-10.588	44.142	1.00	19.15
3913	CB	HIS	A	615	60.472	-12.330	45.226	1.00	19.79
3914	CG	HIS	A	615	61.244	-13.480	45.789	1.00	21.80
3915	ND1	HIS	A	615	61.349	-13.681	47.151	1.00	22.61
3916	CD2	HIS	A	615	62.034	-14.415	45.189	1.00	23.99
3917	CE1	HIS	A	615	62.102	-14.765	47.345	1.00	24.07
3918	NE2	HIS	A	615	62.561	-15.201	46.179	1.00	24.55
3919	N	VAL	A	616	59.898	-10.221	42.256	1.00	19.10
3920	CA	VAL	A	616	59.090	-9.071	41.856	1.00	18.87
3921	C	VAL	A	616	57.723	-9.605	41.412	1.00	18.87
3922	O	VAL	A	616	57.590	-10.767	41.010	1.00	16.35
3923	CB	VAL	A	616	59.829	-8.264	40.774	1.00	21.79
3924	CG1	VAL	A	616	61.242	-7.865	41.282	1.00	19.85
3925	CG2	VAL	A	616	59.980	-9.080	39.511	1.00	22.01
3926	N	ASP	A	617	56.694	-8.777	41.512	1.00	16.55
3927	CA	ASP	A	617	55.309	-9.174	41.337	1.00	17.29
3928	C	ASP	A	617	54.694	-8.774	39.989	1.00	17.05
3929	O	ASP	A	617	53.493	-9.039	39.778	1.00	14.04
3930	CB	ASP	A	617	54.484	-8.457	42.450	1.00	15.59
3931	CG	ASP	A	617	55.057	-8.762	43.825	1.00	18.73
3932	OD1	ASP	A	617	55.655	-7.918	44.531	1.00	18.45
3933	OD2	ASP	A	617	54.889	-9.919	44.243	1.00	17.15

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3934	N	GLY A 618	55.464	-8.049	39.176	1.00	15.87
3935	CA	GLY A 618	54.873	-7.628	37.888	1.00	16.30
3936	C	GLY A 618	55.813	-6.711	37.149	1.00	15.89
3937	O	GLY A 618	56.907	-6.366	37.645	1.00	16.86
3938	N	PHE A 619	55.484	-6.362	35.912	1.00	15.02
3939	CA	PHE A 619	56.312	-5.472	35.083	1.00	14.50
3940	C	PHE A 619	55.488	-4.376	34.420	1.00	15.17
3941	O	PHE A 619	54.403	-4.681	33.856	1.00	13.52
3942	CB	PHE A 619	56.997	-6.325	33.956	1.00	14.48
3943	CG	PHE A 619	58.073	-7.230	34.506	1.00	16.81
3944	CD1	PHE A 619	59.281	-6.690	34.973	1.00	16.56
3945	CD2	PHE A 619	57.858	-8.593	34.669	1.00	16.67
3946	CE1	PHE A 619	60.255	-7.484	35.545	1.00	15.02
3947	CE2	PHE A 619	58.854	-9.403	35.213	1.00	15.82
3948	CZ	PHE A 619	60.044	-8.841	35.642	1.00	15.77
3949	N	ARG A 620	56.013	-3.165	34.311	1.00	13.06
3950	CA	ARG A 620	55.491	-2.106	33.449	1.00	14.20
3951	C	ARG A 620	56.455	-1.959	32.251	1.00	13.44
3952	O	ARG A 620	57.627	-1.593	32.444	1.00	12.26
3953	CB	ARG A 620	55.343	-0.758	34.177	1.00	14.29
3954	CG	ARG A 620	55.098	0.479	33.294	1.00	14.46
3955	CD	ARG A 620	56.325	1.383	33.136	1.00	15.20
3956	NE	ARG A 620	55.937	2.660	32.513	1.00	16.32
3957	CZ	ARG A 620	56.625	3.360	31.605	1.00	17.13
3958	NH1	ARG A 620	57.796	2.947	31.125	1.00	13.61
3959	NH2	ARG A 620	56.155	4.529	31.132	1.00	15.70
3960	N	PHE A 621	56.083	-2.274	31.031	1.00	14.29
3961	CA	PHE A 621	56.956	-2.250	29.884	1.00	16.71
3962	C	PHE A 621	56.956	-0.918	29.145	1.00	17.64
3963	O	PHE A 621	55.903	-0.563	28.593	1.00	16.47
3964	CB	PHE A 621	56.636	-3.381	28.868	1.00	17.26
3965	CG	PHE A 621	56.868	-4.750	29.455	1.00	17.89
3966	CD1	PHE A 621	58.079	-5.403	29.341	1.00	15.81
3967	CD2	PHE A 621	55.812	-5.373	30.137	1.00	17.10
3968	CE1	PHE A 621	58.263	-6.641	29.911	1.00	16.43
3969	CE2	PHE A 621	56.005	-6.626	30.688	1.00	16.26
3970	CZ	PHE A 621	57.224	-7.266	30.597	1.00	15.91
3971	N	ASP A 622	58.055	-0.182	29.255	1.00	16.73
3972	CA	ASP A 622	58.232	1.100	28.539	1.00	17.39
3973	C	ASP A 622	57.977	0.876	27.031	1.00	17.25
3974	O	ASP A 622	58.434	-0.189	26.565	1.00	14.93
3975	CB	ASP A 622	59.739	1.393	28.604	1.00	16.80
3976	CG	ASP A 622	60.044	2.811	28.095	1.00	18.67
3977	OD1	ASP A 622	59.447	3.734	28.683	1.00	16.60
3978	OD2	ASP A 622	60.871	2.977	27.145	1.00	18.13
3979	N	LEU A 623	57.278	1.764	26.338	1.00	14.28
3980	CA	LEU A 623	56.984	1.619	24.923	1.00	15.86
3981	C	LEU A 623	56.733	0.197	24.536	1.00	15.06
3982	O	LEU A 623	57.346	-0.346	23.597	1.00	16.48
3983	CB	LEU A 623	58.151	2.214	24.052	1.00	14.51
3984	CG	LEU A 623	58.401	3.692	24.416	1.00	16.34
3985	CD1	LEU A 623	59.675	4.160	23.681	1.00	16.33
3986	CD2	LEU A 623	57.188	4.593	24.089	1.00	13.45
3987	N	MET A 624	55.835	-0.489	25.247	1.00	15.49
3988	CA	MET A 624	55.522	-1.877	25.003	1.00	13.19
3989	C	MET A 624	55.102	-2.198	23.584	1.00	16.10
3990	O	MET A 624	55.275	-3.346	23.112	1.00	13.77
3991	CB	MET A 624	54.406	-2.290	25.999	1.00	14.22
3992	CG	MET A 624	54.070	-3.777	26.030	1.00	14.94
3993	SD	MET A 624	52.877	-4.324	27.305	1.00	14.57
3994	CE	MET A 624	51.421	-3.499	26.628	1.00	14.71
3995	N	ALA A 625	54.506	-1.234	22.820	1.00	15.88
3996	CA	ALA A 625	54.068	-1.599	21.477	1.00	16.48
3997	C	ALA A 625	55.250	-2.159	20.679	1.00	16.42
3998	O	ALA A 625	55.086	-3.090	19.890	1.00	14.03
3999	CB	ALA A 625	53.509	-0.409	20.706	1.00	16.88
4000	N	LEU A 626	56.430	-1.596	20.853	1.00	16.65
4001	CA	LEU A 626	57.627	-2.049	20.152	1.00	17.27
4002	C	LEU A 626	58.090	-3.482	20.395	1.00	18.21
4003	O	LEU A 626	58.839	-4.029	19.551	1.00	18.64
4004	CB	LEU A 626	58.766	-1.121	20.566	1.00	17.52
4005	CG	LEU A 626	58.661	0.383	20.154	1.00	17.88
4006	CD1	LEU A 626	59.903	1.092	20.758	1.00	16.85
4007	CD2	LEU A 626	58.680	0.441	18.639	1.00	17.72
4008	N	LEU A 627	57.659	-4.144	21.467	1.00	16.19
4009	CA	LEU A 627	58.113	-5.513	21.759	1.00	15.53
4010	C	LEU A 627	57.363	-6.526	20.913	1.00	16.98
4011	O	LEU A 627	57.855	-7.640	20.681	1.00	17.15
4012	CB	LEU A 627	57.921	-5.793	23.258	1.00	13.38
4013	CG	LEU A 627	58.686	-4.849	24.212	1.00	15.02
4014	CD1	LEU A 627	58.414	-5.232	25.681	1.00	15.03
4015	CD2	LEU A 627	60.170	-4.930	23.934	1.00	14.76
4016	N	GLY A 628	56.185	-6.119	20.421	1.00	17.12
4017	CA	GLY A 628	55.382	-6.956	19.534	1.00	18.12
4018	C	GLY A 628	54.439	-7.946	20.204	1.00	17.72
4019	O	GLY A 628	54.669	-8.439	21.306	1.00	16.57
4020	N	LYS A 629	53.318	-8.265	19.560	1.00	18.93
4021	CA	LYS A 629	52.277	-9.137	20.075	1.00	20.91
4022	C	LYS A 629	52.713	-10.539	20.453	1.00	19.69
4023	O	LYS A 629	52.362	-11.008	21.533	1.00	16.07
4024	CB	LYS A 629	51.156	-9.305	19.012	1.00	25.01
4025	CG	LYS A 629	49.955	-8.430	19.255	1.00	30.66
4026	CD	LYS A 629	48.648	-9.053	18.751	1.00	34.60
4027	CE	LYS A 629	48.662	-9.270	17.249	1.00	36.35
4028	NZ	LYS A 629	47.246	-9.312	16.726	1.00	39.65
4029	N	ASP A 630	53.433	-11.217	19.563	1.00	19.67

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4030	CA	ASP	A	630	53.949	-12.557	19.788	1.00	21.78
4031	C	ASP	A	630	54.931	-12.616	20.960	1.00	19.85
4032	O	ASP	A	630	54.849	-13.490	21.817	1.00	18.70
4033	CB	ASP	A	630	54.660	-13.041	18.517	1.00	26.04
4034	CG	ASP	A	630	53.695	-13.269	17.360	1.00	31.74
4035	OD1	ASP	A	630	54.169	-13.303	16.193	1.00	34.75
4036	OD2	ASP	A	630	52.469	-13.434	17.529	1.00	33.72
4037	N	THR	A	631	55.845	-11.675	21.097	1.00	18.89
4038	CA	THR	A	631	56.697	-11.571	22.286	1.00	17.67
4039	C	THR	A	631	55.928	-11.360	23.584	1.00	17.16
4040	O	THR	A	631	56.197	-12.037	24.596	1.00	17.74
4041	CB	THR	A	631	57.728	-10.455	22.062	1.00	16.84
4042	OG1	THR	A	631	58.509	-10.815	20.895	1.00	16.86
4043	CG2	THR	A	631	58.658	-10.288	23.259	1.00	14.40
4044	N	MET	A	632	54.947	-10.471	23.613	1.00	15.74
4045	CA	MET	A	632	54.128	-10.195	24.787	1.00	16.10
4046	C	MET	A	632	53.304	-11.399	25.193	1.00	17.20
4047	O	MET	A	632	53.196	-11.659	26.389	1.00	16.17
4048	CB	MET	A	632	53.256	-8.950	24.696	1.00	14.99
4049	CG	MET	A	632	53.997	-7.596	24.713	1.00	13.86
4050	SD	MET	A	632	55.378	-7.434	25.863	1.00	14.63
4051	CE	MET	A	632	54.506	-7.782	27.400	1.00	16.56
4052	N	ALA	A	633	52.764	-12.173	24.245	1.00	17.61
4053	CA	ALA	A	633	52.008	-13.370	24.597	1.00	17.78
4054	C	ALA	A	633	52.902	-14.414	25.286	1.00	18.00
4055	O	ALA	A	633	52.463	-15.073	26.245	1.00	15.84
4056	CB	ALA	A	633	51.391	-13.971	23.328	1.00	16.07
4057	N	LYS	A	634	54.135	-14.550	24.791	1.00	18.45
4058	CA	LYS	A	634	55.101	-15.503	25.368	1.00	19.92
4059	C	LYS	A	634	55.571	-15.082	26.757	1.00	19.10
4060	O	LYS	A	634	55.753	-15.910	27.661	1.00	16.95
4061	CB	LYS	A	634	56.365	-15.667	24.495	1.00	21.98
4062	CG	LYS	A	634	56.109	-16.327	23.139	1.00	25.49
4063	CD	LYS	A	634	57.432	-16.789	22.524	1.00	27.52
4064	CE	LYS	A	634	57.239	-17.490	21.173	1.00	27.96
4065	NZ	LYS	A	634	58.537	-17.479	20.413	1.00	29.38
4066	N	ILE	A	635	55.768	-13.775	26.941	1.00	17.02
4067	CA	ILE	A	635	56.142	-13.264	28.263	1.00	17.04
4068	C	ILE	A	635	54.985	-13.581	29.221	1.00	18.26
4069	O	ILE	A	635	55.242	-14.096	30.321	1.00	16.99
4070	CB	ILE	A	635	56.444	-11.752	28.267	1.00	18.88
4071	CG1	ILE	A	635	57.787	-11.462	27.535	1.00	18.51
4072	CG2	ILE	A	635	56.370	-11.171	29.670	1.00	15.03
4073	CD1	ILE	A	635	58.004	-9.955	27.358	1.00	18.80
4074	N	SER	A	636	53.742	-13.211	28.818	1.00	16.75
4075	CA	SER	A	636	52.587	-13.505	29.684	1.00	16.38
4076	C	SER	A	636	52.396	-14.985	29.963	1.00	17.44
4077	O	SER	A	636	52.268	-15.366	31.134	1.00	15.83
4078	CB	SER	A	636	51.327	-12.920	29.022	1.00	17.93
4079	OG	SER	A	636	50.145	-13.262	29.716	1.00	18.44
4080	N	ASN	A	637	52.473	-15.869	28.956	1.00	18.57
4081	CA	ASN	A	637	52.375	-17.314	29.219	1.00	20.52
4082	C	ASN	A	637	53.492	-17.878	30.092	1.00	21.51
4083	O	ASN	A	637	53.154	-18.683	30.984	1.00	22.24
4084	CB	ASN	A	637	52.291	-18.099	27.902	1.00	19.88
4085	CG	ASN	A	637	51.013	-17.754	27.145	1.00	21.97
4086	OD1	ASN	A	637	50.142	-17.046	27.666	1.00	23.68
4087	ND2	ASN	A	637	50.868	-18.237	25.912	1.00	21.76
4088	N	GLU	A	638	54.752	-17.482	29.901	1.00	19.30
4089	CA	GLU	A	638	55.825	-17.997	30.751	1.00	21.15
4090	C	GLU	A	638	55.668	-17.545	32.199	1.00	19.63
4091	O	GLU	A	638	55.839	-18.358	33.122	1.00	19.31
4092	CB	GLU	A	638	57.218	-17.580	30.253	1.00	21.35
4093	CG	GLU	A	638	57.655	-18.382	29.023	1.00	22.98
4094	CD	GLU	A	638	59.094	-18.201	28.573	1.00	24.51
4095	OE1	GLU	A	638	59.324	-18.637	27.404	1.00	24.01
4096	OE2	GLU	A	638	59.978	-17.673	29.315	1.00	22.90
4097	N	LEU	A	639	55.428	-16.257	32.402	1.00	18.27
4098	CA	LEU	A	639	55.291	-15.771	33.784	1.00	19.11
4099	C	LEU	A	639	54.017	-16.268	34.422	1.00	19.62
4100	O	LEU	A	639	54.073	-16.629	35.613	1.00	19.57
4101	CB	LEU	A	639	55.454	-14.237	33.905	1.00	17.12
4102	CG	LEU	A	639	56.786	-13.720	33.342	1.00	17.07
4103	CD1	LEU	A	639	56.903	-12.195	33.297	1.00	15.55
4104	CD2	LEU	A	639	57.975	-14.331	34.093	1.00	16.23
4105	N	HIS	A	640	52.879	-16.404	33.716	1.00	19.06
4106	CA	HIS	A	640	51.679	-16.908	34.394	1.00	20.34
4107	C	HIS	A	640	51.739	-18.383	34.784	1.00	22.10
4108	O	HIS	A	640	50.969	-18.816	35.671	1.00	21.35
4109	CB	HIS	A	640	50.420	-16.629	33.582	1.00	19.39
4110	CG	HIS	A	640	50.102	-15.160	33.517	1.00	20.54
4111	ND1	HIS	A	640	50.217	-14.293	34.601	1.00	19.70
4112	CD2	HIS	A	640	49.610	-14.433	32.483	1.00	18.57
4113	CE1	HIS	A	640	49.752	-13.097	34.246	1.00	18.71
4114	NE2	HIS	A	640	49.412	-13.172	32.965	1.00	19.82
4115	N	ALA	A	641	52.612	-19.173	34.200	1.00	23.98
4116	CA	ALA	A	641	52.801	-20.579	34.579	1.00	26.49
4117	C	ALA	A	641	53.598	-20.615	35.882	1.00	27.89
4118	O	ALA	A	641	53.510	-21.587	36.628	1.00	31.74
4119	CB	ALA	A	641	53.605	-21.327	33.512	1.00	26.50
4120	N	ILE	A	642	54.437	-19.626	36.174	1.00	28.13
4121	CA	ILE	A	642	55.107	-19.555	37.476	1.00	29.40
4122	C	ILE	A	642	54.093	-19.073	38.530	1.00	28.86
4123	O	ILE	A	642	53.932	-19.665	39.596	1.00	26.64
4124	CB	ILE	A	642	56.310	-18.608	37.450	1.00	29.90
4125	CG1	ILE	A	642	57.312	-18.997	36.344	1.00	30.38

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4126	CG2	ILE	A	642	57.009	-18.615	38.817	1.00	30.02
4127	CD1	ILE	A	642	58.394	-17.943	36.170	1.00	30.48
4128	N	ASN	A	643	53.361	-17.993	38.188	1.00	26.34
4129	CA	ASN	A	643	52.345	-17.452	39.112	1.00	23.82
4130	C	ASN	A	643	51.282	-16.700	38.316	1.00	24.17
4131	O	ASN	A	643	51.544	-15.628	37.774	1.00	21.45
4132	CB	ASN	A	643	53.051	-16.543	40.122	1.00	22.05
4133	CG	ASN	A	643	52.079	-15.861	41.083	1.00	23.41
4134	OD1	ASN	A	643	50.871	-16.089	41.037	1.00	21.01
4135	ND2	ASN	A	643	52.555	-15.009	41.966	1.00	22.58
4136	N	PRO	A	644	50.049	-17.213	38.277	1.00	23.33
4137	CA	PRO	A	644	48.956	-16.613	37.531	1.00	22.06
4138	C	PRO	A	644	48.572	-15.222	37.983	1.00	19.69
4139	O	PRO	A	644	47.936	-14.499	37.220	1.00	20.72
4140	CB	PRO	A	644	47.775	-17.582	37.713	1.00	23.07
4141	CG	PRO	A	644	48.101	-18.344	38.959	1.00	24.32
4142	CD	PRO	A	644	49.621	-18.473	38.945	1.00	23.67
4143	N	GLY	A	645	48.892	-14.797	39.190	1.00	18.01
4144	CA	GLY	A	645	48.637	-13.494	39.741	1.00	17.70
4145	C	GLY	A	645	49.592	-12.380	39.283	1.00	19.60
4146	O	GLY	A	645	49.390	-11.193	39.628	1.00	15.48
4147	N	ILE	A	646	50.660	-12.723	38.538	1.00	18.09
4148	CA	ILE	A	646	51.643	-11.732	38.106	1.00	17.16
4149	C	ILE	A	646	50.986	-10.704	37.203	1.00	16.23
4150	O	ILE	A	646	50.260	-11.076	36.307	1.00	17.07
4151	CB	ILE	A	646	52.885	-12.409	37.477	1.00	17.81
4152	CG1	ILE	A	646	53.818	-12.981	38.569	1.00	18.48
4153	CG2	ILE	A	646	53.723	-11.434	36.653	1.00	17.45
4154	CD1	ILE	A	646	54.986	-13.812	38.061	1.00	16.75
4155	N	VAL	A	647	51.202	-9.403	37.398	1.00	16.03
4156	CA	VAL	A	647	50.549	-8.329	36.668	1.00	15.29
4157	C	VAL	A	647	51.490	-7.688	35.644	1.00	16.91
4158	O	VAL	A	647	52.608	-7.229	35.981	1.00	14.67
4159	CB	VAL	A	647	50.020	-7.276	37.651	1.00	16.53
4160	CG1	VAL	A	647	49.281	-6.165	36.945	1.00	15.28
4161	CG2	VAL	A	647	49.094	-7.913	38.727	1.00	15.02
4162	N	LEU	A	648	51.048	-7.688	34.392	1.00	13.55
4163	CA	LEU	A	648	51.862	-7.214	33.256	1.00	16.97
4164	C	LEU	A	648	51.149	-6.179	32.396	1.00	17.87
4165	O	LEU	A	648	49.993	-6.422	32.031	1.00	18.62
4166	CB	LEU	A	648	52.123	-8.454	32.390	1.00	14.99
4167	CG	LEU	A	648	52.778	-9.673	33.034	1.00	14.65
4168	CD1	LEU	A	648	52.716	-10.926	32.153	1.00	12.97
4169	CD2	LEU	A	648	54.247	-9.321	33.383	1.00	12.67
4170	N	TYR	A	649	51.744	-5.012	32.124	1.00	17.59
4171	CA	TYR	A	649	51.053	-3.961	31.359	1.00	17.71
4172	C	TYR	A	649	52.086	-3.025	30.737	1.00	18.28
4173	O	TYR	A	649	53.272	-3.151	31.086	1.00	18.59
4174	CB	TYR	A	649	50.082	-3.164	32.269	1.00	14.25
4175	CG	TYR	A	649	50.752	-2.654	33.527	1.00	13.60
4176	CD1	TYR	A	649	50.833	-3.456	34.665	1.00	14.53
4177	CD2	TYR	A	649	51.240	-1.358	33.610	1.00	11.51
4178	CE1	TYR	A	649	51.501	-3.023	35.819	1.00	13.05
4179	CE2	TYR	A	649	51.869	-0.891	34.758	1.00	13.13
4180	CZ	TYR	A	649	52.001	-1.743	35.853	1.00	14.34
4181	OH	TYR	A	649	52.639	-1.254	36.972	1.00	11.99
4182	N	GLY	A	650	51.670	-2.046	29.915	1.00	18.09
4183	CA	GLY	A	650	52.684	-1.112	29.378	1.00	16.66
4184	C	GLY	A	650	52.088	-0.094	28.439	1.00	17.73
4185	O	GLY	A	650	50.851	-0.034	28.270	1.00	16.48
4186	N	GLU	A	651	52.922	0.800	27.876	1.00	17.53
4187	CA	GLU	A	651	52.431	1.880	27.026	1.00	17.39
4188	C	GLU	A	651	52.077	1.368	25.620	1.00	17.53
4189	O	GLU	A	651	52.976	0.899	24.910	1.00	19.12
4190	CB	GLU	A	651	53.546	2.926	26.950	1.00	19.60
4191	CG	GLU	A	651	53.976	3.596	28.238	1.00	20.41
4192	CD	GLU	A	651	55.141	4.573	28.068	1.00	22.59
4193	OE1	GLU	A	651	56.242	4.141	27.636	1.00	18.94
4194	OE2	GLU	A	651	54.935	5.780	28.390	1.00	20.69
4195	N	PRO	A	652	50.856	1.556	25.122	1.00	17.10
4196	CA	PRO	A	652	50.515	1.043	23.784	1.00	18.38
4197	C	PRO	A	652	50.940	1.945	22.648	1.00	18.28
4198	O	PRO	A	652	50.125	2.221	21.773	1.00	19.43
4199	CB	PRO	A	652	48.957	0.908	23.883	1.00	17.61
4200	CG	PRO	A	652	48.591	2.087	24.748	1.00	16.44
4201	CD	PRO	A	652	49.695	2.112	25.852	1.00	15.52
4202	N	TRP	A	653	52.098	2.594	22.614	1.00	18.69
4203	CA	TRP	A	653	52.549	3.503	21.554	1.00	18.43
4204	C	TRP	A	653	54.065	3.398	21.359	1.00	17.97
4205	O	TRP	A	653	54.779	2.764	22.137	1.00	15.71
4206	CB	TRP	A	653	52.091	4.950	21.814	1.00	19.02
4207	CG	TRP	A	653	52.439	5.531	23.150	1.00	18.75
4208	CD1	TRP	A	653	53.669	5.991	23.523	1.00	20.11
4209	CD2	TRP	A	653	51.603	5.706	24.308	1.00	20.38
4210	NE1	TRP	A	653	53.655	6.453	24.824	1.00	20.51
4211	CE2	TRP	A	653	52.378	6.290	25.318	1.00	20.60
4212	CE3	TRP	A	653	50.242	5.446	24.554	1.00	19.16
4213	CZ2	TRP	A	653	51.869	6.584	26.595	1.00	22.37
4214	CZ3	TRP	A	653	49.738	5.760	25.813	1.00	19.76
4215	CH2	TRP	A	653	50.542	6.323	26.813	1.00	20.77
4216	N	THR	A	654	54.658	4.006	20.338	1.00	17.06
4217	CA	THR	A	654	56.072	4.010	20.058	1.00	18.41
4218	C	THR	A	654	56.620	5.431	20.270	1.00	19.84
4219	O	THR	A	654	55.835	6.339	20.572	1.00	20.60
4220	CB	THR	A	654	56.438	3.591	18.608	1.00	19.02
4221	OG1	THR	A	654	56.079	4.691	17.734	1.00	18.49

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4222	CG2	THR	A	654	55.687	2.359	18.174	1.00	16.83
4223	N	GLY	A	655	57.916	5.601	20.196	1.00	21.18
4224	CA	GLY	A	655	58.633	6.858	20.389	1.00	21.26
4225	C	GLY	A	655	58.929	7.605	19.077	1.00	24.38
4226	O	GLY	A	655	58.912	8.849	19.015	1.00	24.84
4227	N	GLY	A	656	59.178	6.896	18.002	1.00	22.39
4228	CA	GLY	A	656	59.338	7.387	16.658	1.00	24.45
4229	C	GLY	A	656	58.840	6.337	15.661	1.00	25.22
4230	O	GLY	A	656	58.050	5.459	16.055	1.00	25.29
4231	N	THR	A	657	59.280	6.365	14.403	1.00	23.11
4232	CA	THR	A	657	58.848	5.425	13.380	1.00	23.56
4233	C	THR	A	657	59.546	4.082	13.588	1.00	22.19
4234	O	THR	A	657	60.759	4.098	13.820	1.00	20.73
4235	CB	THR	A	657	59.256	5.972	11.983	1.00	26.11
4236	OG1	THR	A	657	58.698	7.292	11.803	1.00	27.58
4237	CG2	THR	A	657	58.669	5.066	10.912	1.00	26.30
4238	N	SER	A	658	58.846	2.963	13.574	1.00	22.05
4239	CA	SER	A	658	59.408	1.688	13.981	1.00	22.49
4240	C	SER	A	658	59.740	0.805	12.779	1.00	23.91
4241	O	SER	A	658	58.952	0.966	11.879	1.00	21.76
4242	CB	SER	A	658	58.435	0.890	14.874	1.00	22.19
4243	OG	SER	A	658	59.035	-0.398	15.133	1.00	20.61
4244	N	GLY	A	659	60.747	-0.101	12.852	1.00	22.44
4245	CA	GLY	A	659	60.886	-1.041	11.765	1.00	22.70
4246	C	GLY	A	659	59.939	-2.211	11.917	1.00	24.64
4247	O	GLY	A	659	59.836	-3.016	10.967	1.00	25.07
4248	N	LEU	A	660	59.245	-2.383	13.049	1.00	22.82
4249	CA	LEU	A	660	58.349	-3.534	13.163	1.00	22.64
4250	C	LEU	A	660	57.049	-3.271	12.408	1.00	24.58
4251	O	LEU	A	660	56.462	-2.191	12.541	1.00	23.39
4252	CB	LEU	A	660	58.032	-3.798	14.656	1.00	21.87
4253	CG	LEU	A	660	57.221	-5.073	14.921	1.00	21.46
4254	CD1	LEU	A	660	58.005	-6.333	14.553	1.00	21.53
4255	CD2	LEU	A	660	56.796	-5.118	16.387	1.00	22.01
4256	N	SER	A	661	56.498	-4.299	11.768	1.00	28.28
4257	CA	SER	A	661	55.249	-4.110	11.039	1.00	31.06
4258	C	SER	A	661	54.123	-3.721	11.988	1.00	31.92
4259	O	SER	A	661	53.977	-4.115	13.149	1.00	30.73
4260	CB	SER	A	661	54.841	-5.369	10.278	1.00	33.28
4261	OG	SER	A	661	54.406	-6.282	11.303	1.00	38.97
4262	N	SER	A	662	53.207	-2.944	11.425	1.00	31.42
4263	CA	SER	A	662	52.040	-2.489	12.154	1.00	31.08
4264	C	SER	A	662	51.177	-3.592	12.719	1.00	30.70
4265	O	SER	A	662	50.577	-3.441	13.808	1.00	29.15
4266	CB	SER	A	662	51.250	-1.605	11.179	1.00	33.72
4267	OG	SER	A	662	50.239	-0.982	11.936	1.00	37.74
4268	N	ASP	A	663	51.069	-4.738	12.047	1.00	29.07
4269	CA	ASP	A	663	50.244	-5.830	12.522	1.00	30.96
4270	C	ASP	A	663	50.781	-6.442	13.814	1.00	27.66
4271	O	ASP	A	663	50.053	-7.210	14.429	1.00	24.98
4272	CB	ASP	A	663	50.219	-6.998	11.510	1.00	37.98
4273	CG	ASP	A	663	50.022	-6.418	10.118	1.00	43.25
4274	OD1	ASP	A	663	51.041	-6.067	9.479	1.00	46.25
4275	OD2	ASP	A	663	48.826	-6.288	9.774	1.00	46.03
4276	N	GLN	A	664	52.066	-6.234	14.108	1.00	22.67
4277	CA	GLN	A	664	52.601	-6.838	15.333	1.00	23.37
4278	C	GLN	A	664	52.675	-5.789	16.432	1.00	22.24
4279	O	GLN	A	664	52.822	-6.210	17.585	1.00	19.91
4280	CB	GLN	A	664	53.947	-7.514	15.015	1.00	23.40
4281	CG	GLN	A	664	53.799	-8.961	14.521	1.00	24.74
4282	CD	GLN	A	664	53.177	-9.871	15.593	1.00	25.49
4283	OE1	GLN	A	664	53.749	-9.992	16.703	1.00	24.23
4284	NE2	GLN	A	664	52.036	-10.506	15.305	1.00	23.12
4285	N	LEU	A	665	52.600	-4.486	16.125	1.00	19.96
4286	CA	LEU	A	665	52.740	-3.486	17.200	1.00	19.39
4287	C	LEU	A	665	51.651	-3.648	18.238	1.00	18.71
4288	O	LEU	A	665	50.488	-3.843	17.884	1.00	17.87
4289	CB	LEU	A	665	52.765	-2.046	16.656	1.00	20.03
4290	CG	LEU	A	665	53.973	-1.662	15.786	1.00	21.89
4291	CD1	LEU	A	665	53.709	-0.411	14.951	1.00	20.88
4292	CD2	LEU	A	665	55.207	-1.501	16.668	1.00	22.05
4293	N	VAL	A	666	51.929	-3.519	19.533	1.00	18.78
4294	CA	VAL	A	666	50.885	-3.678	20.558	1.00	18.52
4295	C	VAL	A	666	50.237	-2.321	20.883	1.00	19.69
4296	O	VAL	A	666	50.466	-1.789	21.955	1.00	17.22
4297	CB	VAL	A	666	51.359	-4.354	21.835	1.00	16.96
4298	CG1	VAL	A	666	50.206	-4.834	22.723	1.00	19.29
4299	CG2	VAL	A	666	52.295	-5.532	21.529	1.00	14.78
4300	N	THR	A	667	49.290	-1.919	20.033	1.00	20.48
4301	CA	THR	A	667	48.502	-0.702	20.179	1.00	20.14
4302	C	THR	A	667	47.197	-1.024	20.902	1.00	18.13
4303	O	THR	A	667	46.985	-2.227	21.117	1.00	16.98
4304	CB	THR	A	667	48.269	-0.014	18.814	1.00	21.55
4305	OG1	THR	A	667	47.843	-1.044	17.925	1.00	20.10
4306	CG2	THR	A	667	49.597	0.611	18.281	1.00	21.18
4307	N	LYS	A	668	46.331	-0.058	21.255	1.00	16.86
4308	CA	LYS	A	668	45.140	-0.468	22.022	1.00	18.52
4309	C	LYS	A	668	44.229	-1.401	21.234	1.00	19.25
4310	O	LYS	A	668	43.936	-1.077	20.104	1.00	15.25
4311	CB	LYS	A	668	44.277	0.724	22.546	1.00	17.82
4312	CG	LYS	A	668	45.148	1.580	23.472	1.00	19.27
4313	CD	LYS	A	668	44.324	2.507	24.357	1.00	22.35
4314	CE	LYS	A	668	43.581	3.587	23.574	1.00	22.93
4315	NZ	LYS	A	668	44.581	4.231	22.654	1.00	24.34
4316	N	GLY	A	669	43.759	-2.439	21.897	1.00	20.04
4317	CA	GLY	A	669	42.938	-3.451	21.239	1.00	20.82

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4318	C	GLY	A	669	43.782	-4.704	20.955	1.00 21.65
4319	O	GLY	A	669	43.213	-5.800	20.927	1.00 21.36
4320	N	GLN	A	670	45.088	-4.594	20.719	1.00 20.53
4321	CA	GLN	A	670	45.919	-5.759	20.428	1.00 21.35
4322	C	GLN	A	670	46.297	-6.586	21.642	1.00 20.10
4323	O	GLN	A	670	46.749	-7.720	21.456	1.00 19.47
4324	CB	GLN	A	670	47.247	-5.387	19.714	1.00 21.19
4325	CG	GLN	A	670	46.970	-4.705	18.368	1.00 27.47
4326	CD	GLN	A	670	46.169	-5.614	17.439	1.00 31.69
4327	OE1	GLN	A	670	46.616	-6.684	17.021	1.00 32.50
4328	NE2	GLN	A	670	44.937	-5.233	17.073	1.00 34.39
4329	N	GLN	A	671	45.972	-6.145	22.858	1.00 19.44
4330	CA	GLN	A	671	46.228	-6.920	24.059	1.00 19.31
4331	C	GLN	A	671	45.108	-7.890	24.371	1.00 19.04
4332	O	GLN	A	671	45.181	-8.640	25.368	1.00 19.01
4333	CB	GLN	A	671	46.423	-5.943	25.252	1.00 18.95
4334	CG	GLN	A	671	45.140	-5.479	25.924	1.00 18.55
4335	CD	GLN	A	671	44.177	-4.651	25.083	1.00 18.72
4336	OE1	GLN	A	671	42.932	-4.761	25.238	1.00 19.28
4337	NE2	GLN	A	671	44.667	-3.817	24.177	1.00 15.65
4338	N	LYS	A	672	43.957	-7.772	23.698	1.00 17.47
4339	CA	LYS	A	672	42.772	-8.535	24.053	1.00 18.28
4340	C	LYS	A	672	43.062	-10.006	24.247	1.00 17.84
4341	O	LYS	A	672	43.624	-10.599	23.339	1.00 17.28
4342	CB	LYS	A	672	41.622	-8.448	23.030	1.00 21.13
4343	CG	LYS	A	672	40.888	-7.108	22.987	1.00 22.83
4344	CD	LYS	A	672	39.854	-7.147	21.817	1.00 27.44
4345	CE	LYS	A	672	38.826	-6.074	22.145	1.00 30.81
4346	NZ	LYS	A	672	37.962	-5.616	21.015	1.00 33.27
4347	N	GLY	A	673	42.644	-10.575	25.384	1.00 17.84
4348	CA	GLY	A	673	42.889	-11.973	25.692	1.00 16.83
4349	C	GLY	A	673	44.324	-12.396	25.938	1.00 17.57
4350	O	GLY	A	673	44.584	-13.612	26.132	1.00 16.05
4351	N	LEU	A	674	45.337	-11.535	26.003	1.00 16.87
4352	CA	LEU	A	674	46.707	-12.002	26.224	1.00 17.22
4353	C	LEU	A	674	47.121	-12.089	27.692	1.00 18.69
4354	O	LEU	A	674	48.214	-12.614	27.992	1.00 16.27
4355	CB	LEU	A	674	47.688	-11.070	25.482	1.00 16.47
4356	CG	LEU	A	674	47.491	-10.955	23.957	1.00 17.85
4357	CD1	LEU	A	674	48.601	-10.153	23.292	1.00 17.96
4358	CD2	LEU	A	674	47.402	-12.356	23.376	1.00 17.89
4359	N	GLY	A	675	46.351	-11.448	28.580	1.00 17.76
4360	CA	GLY	A	675	46.690	-11.447	29.992	1.00 18.55
4361	C	GLY	A	675	47.533	-10.238	30.385	1.00 18.93
4362	O	GLY	A	675	48.418	-10.331	31.244	1.00 17.89
4363	N	ILE	A	676	47.527	-9.199	29.566	1.00 18.34
4364	CA	ILE	A	676	48.279	-7.984	29.777	1.00 18.64
4365	C	ILE	A	676	47.341	-6.773	29.627	1.00 17.75
4366	O	ILE	A	676	46.311	-6.893	28.941	1.00 16.31
4367	CB	ILE	A	676	49.479	-7.831	28.825	1.00 19.70
4368	CG1	ILE	A	676	49.028	-7.552	27.392	1.00 20.32
4369	CG2	ILE	A	676	50.426	-9.050	28.832	1.00 17.85
4370	CD1	ILE	A	676	50.167	-7.324	26.394	1.00 17.85
4371	N	GLY	A	677	47.751	-5.639	30.156	1.00 13.65
4372	CA	GLY	A	677	47.021	-4.394	30.070	1.00 15.81
4373	C	GLY	A	677	47.769	-3.254	29.403	1.00 16.01
4374	O	GLY	A	677	48.991	-3.301	29.151	1.00 16.11
4375	N	VAL	A	678	47.038	-2.172	29.079	1.00 15.57
4376	CA	VAL	A	678	47.638	-1.027	28.427	1.00 15.53
4377	C	VAL	A	678	47.199	0.251	29.119	1.00 16.70
4378	O	VAL	A	678	46.014	0.364	29.518	1.00 18.08
4379	CB	VAL	A	678	47.310	-0.949	26.919	1.00 14.79
4380	CG1	VAL	A	678	47.819	-2.120	26.065	1.00 16.01
4381	CG2	VAL	A	678	45.761	-0.920	26.704	1.00 15.88
4382	N	PHE	A	679	48.111	1.185	29.240	1.00 12.93
4383	CA	PHE	A	679	47.799	2.494	29.790	1.00 13.80
4384	C	PHE	A	679	46.705	3.036	28.866	1.00 16.99
4385	O	PHE	A	679	46.830	3.061	27.626	1.00 16.58
4386	CB	PHE	A	679	49.075	3.354	29.813	1.00 15.10
4387	CG	PHE	A	679	49.992	3.064	30.997	1.00 16.37
4388	CD1	PHE	A	679	51.234	2.485	30.823	1.00 17.10
4389	CD2	PHE	A	679	49.591	3.420	32.282	1.00 15.14
4390	CE1	PHE	A	679	52.097	2.258	31.903	1.00 17.80
4391	CE2	PHE	A	679	50.451	3.191	33.364	1.00 17.84
4392	CZ	PHE	A	679	51.687	2.594	33.195	1.00 16.20
4393	N	ASN	A	680	45.614	3.469	29.502	1.00 17.15
4394	CA	ASN	A	680	44.468	3.996	28.753	1.00 16.69
4395	C	ASN	A	680	44.612	5.491	28.529	1.00 16.69
4396	O	ASN	A	680	44.157	6.287	29.363	1.00 15.66
4397	CB	ASN	A	680	43.205	3.658	29.584	1.00 15.17
4398	CG	ASN	A	680	41.905	4.021	28.891	1.00 16.39
4399	OD1	ASN	A	680	40.786	3.672	29.326	1.00 19.69
4400	ND2	ASN	A	680	41.946	4.799	27.835	1.00 13.35
4401	N	ASP	A	681	45.204	5.905	27.392	1.00 15.34
4402	CA	ASP	A	681	45.322	7.314	27.098	1.00 17.64
4403	C	ASP	A	681	43.983	7.925	26.684	1.00 15.96
4404	O	ASP	A	681	43.930	9.146	26.750	1.00 18.29
4405	CB	ASP	A	681	46.434	7.675	26.088	1.00 16.68
4406	CG	ASP	A	681	46.314	6.929	24.779	1.00 20.08
4407	OD1	ASP	A	681	45.917	5.745	24.708	1.00 18.82
4408	OD2	ASP	A	681	46.590	7.570	23.728	1.00 21.03
4409	N	ASN	A	682	42.939	7.183	26.388	1.00 16.19
4410	CA	ASN	A	682	41.626	7.732	26.064	1.00 16.30
4411	C	ASN	A	682	41.008	8.391	27.314	1.00 17.28
4412	O	ASN	A	682	40.543	9.554	27.320	1.00 16.98
4413	CB	ASN	A	682	40.706	6.629	25.496	1.00 15.40

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4414	CG	ASN	A	682	41.010	6.205	24.062	1.00	17.13
4415	OD1	ASN	A	682	41.866	6.815	23.416	1.00	16.74
4416	ND2	ASN	A	682	40.350	5.175	23.511	1.00	15.15
4417	N	ILE	A	683	41.032	7.677	28.454	1.00	16.35
4418	CA	ILE	A	683	40.470	8.220	29.694	1.00	16.07
4419	C	ILE	A	683	41.284	9.380	30.251	1.00	17.30
4420	O	ILE	A	683	40.836	10.455	30.737	1.00	17.55
4421	CB	ILE	A	683	40.228	7.122	30.748	1.00	16.73
4422	CG1	ILE	A	683	39.118	7.666	31.683	1.00	17.76
4423	CG2	ILE	A	683	41.474	6.693	31.535	1.00	13.77
4424	CD1	ILE	A	683	38.930	6.930	32.986	1.00	18.13
4425	N	ARG	A	684	42.600	9.261	30.064	1.00	15.73
4426	CA	ARG	A	684	43.514	10.306	30.488	1.00	16.66
4427	C	ARG	A	684	43.207	11.587	29.736	1.00	15.87
4428	O	ARG	A	684	43.115	12.677	30.317	1.00	16.71
4429	CB	ARG	A	684	44.976	9.857	30.262	1.00	18.05
4430	CG	ARG	A	684	45.952	10.905	30.788	1.00	20.35
4431	CD	ARG	A	684	47.222	11.054	30.003	1.00	26.33
4432	NE	ARG	A	684	47.113	11.061	28.560	1.00	30.02
4433	CZ	ARG	A	684	48.001	10.589	27.682	1.00	32.36
4434	NH1	ARG	A	684	49.205	10.033	27.964	1.00	33.59
4435	NH2	ARG	A	684	47.644	10.673	26.404	1.00	33.28
4436	N	ASN	A	685	43.193	11.515	28.410	1.00	15.54
4437	CA	ASN	A	685	42.944	12.721	27.596	1.00	17.75
4438	C	ASN	A	685	41.554	13.294	27.914	1.00	16.60
4439	O	ASN	A	685	41.377	14.510	27.960	1.00	16.32
4440	CB	ASN	A	685	43.101	12.404	26.078	1.00	15.79
4441	CG	ASN	A	685	44.559	12.204	25.670	1.00	17.29
4442	OD1	ASN	A	685	45.564	12.731	26.189	1.00	15.27
4443	ND2	ASN	A	685	44.757	11.357	24.661	1.00	18.75
4444	N	GLY	A	686	40.581	12.454	28.172	1.00	16.82
4445	CA	GLY	A	686	39.208	12.841	28.482	1.00	18.79
4446	C	GLY	A	686	39.085	13.538	29.825	1.00	18.90
4447	O	GLY	A	686	38.321	14.506	29.982	1.00	18.03
4448	N	LEU	A	687	39.870	13.071	30.804	1.00	18.75
4449	CA	LEU	A	687	39.858	13.683	32.131	1.00	17.87
4450	C	LEU	A	687	40.445	15.084	32.155	1.00	19.56
4451	O	LEU	A	687	39.835	15.949	32.801	1.00	18.35
4452	CB	LEU	A	687	40.553	12.740	33.143	1.00	17.50
4453	CG	LEU	A	687	39.691	11.524	33.514	1.00	16.49
4454	CD1	LEU	A	687	40.525	10.497	34.266	1.00	15.82
4455	CD2	LEU	A	687	38.459	11.960	34.349	1.00	17.74
4456	N	ASP	A	688	41.590	15.386	31.529	1.00	19.00
4457	CA	ASP	A	688	42.114	16.743	31.606	1.00	19.09
4458	C	ASP	A	688	42.632	17.315	30.289	1.00	18.61
4459	O	ASP	A	688	43.299	18.348	30.374	1.00	17.40
4460	CB	ASP	A	688	43.247	16.843	32.624	1.00	21.76
4461	CG	ASP	A	688	44.491	16.033	32.362	1.00	25.24
4462	OD1	ASP	A	688	44.577	15.205	31.412	1.00	26.02
4463	OD2	ASP	A	688	45.452	16.200	33.160	1.00	24.89
4464	N	GLY	A	689	42.237	16.788	29.143	1.00	19.33
4465	CA	GLY	A	689	42.679	17.411	27.872	1.00	20.12
4466	C	GLY	A	689	43.852	16.650	27.244	1.00	21.08
4467	O	GLY	A	689	44.631	15.975	27.940	1.00	18.25
4468	N	ASN	A	690	43.957	16.778	25.912	1.00	20.39
4469	CA	ASN	A	690	45.008	16.103	25.159	1.00	18.52
4470	C	ASN	A	690	46.382	16.400	25.702	1.00	18.62
4471	O	ASN	A	690	46.767	17.560	25.942	1.00	18.86
4472	CB	ASN	A	690	44.883	16.503	23.659	1.00	20.87
4473	CG	ASN	A	690	45.899	15.668	22.877	1.00	22.43
4474	OD1	ASN	A	690	47.036	16.114	22.664	1.00	22.38
4475	ND2	ASN	A	690	45.472	14.460	22.513	1.00	21.21
4476	N	VAL	A	691	47.256	15.408	25.828	1.00	17.79
4477	CA	VAL	A	691	48.582	15.528	26.410	1.00	20.26
4478	C	VAL	A	691	49.536	16.419	25.616	1.00	20.63
4479	O	VAL	A	691	50.503	16.940	26.182	1.00	19.98
4480	CB	VAL	A	691	49.204	14.114	26.594	1.00	21.95
4481	CG1	VAL	A	691	49.485	13.451	25.233	1.00	19.94
4482	CG2	VAL	A	691	50.487	14.150	27.404	1.00	21.70
4483	N	PHE	A	692	49.287	16.668	24.331	1.00	19.63
4484	CA	PHE	A	692	50.187	17.533	23.544	1.00	20.10
4485	C	PHE	A	692	49.799	19.008	23.561	1.00	18.56
4486	O	PHE	A	692	50.399	19.821	22.869	1.00	18.61
4487	CB	PHE	A	692	50.238	17.053	22.090	1.00	18.53
4488	CG	PHE	A	692	50.859	15.694	21.969	1.00	21.54
4489	CD1	PHE	A	692	50.085	14.538	21.907	1.00	20.75
4490	CD2	PHE	A	692	52.245	15.579	21.964	1.00	21.43
4491	CE1	PHE	A	692	50.723	13.309	21.812	1.00	21.57
4492	CE2	PHE	A	692	52.865	14.348	21.891	1.00	21.34
4493	CZ	PHE	A	692	52.097	13.205	21.793	1.00	21.14
4494	N	ASP	A	693	48.780	19.382	24.314	1.00	19.75
4495	CA	ASP	A	693	48.307	20.760	24.442	1.00	18.18
4496	C	ASP	A	693	48.252	21.124	25.925	1.00	20.25
4497	O	ASP	A	693	47.300	20.850	26.671	1.00	15.97
4498	CB	ASP	A	693	46.932	20.849	23.734	1.00	20.28
4499	CG	ASP	A	693	46.336	22.240	23.779	1.00	22.51
4500	OD1	ASP	A	693	45.186	22.441	23.333	1.00	24.25
4501	OD2	ASP	A	693	47.013	23.154	24.306	1.00	23.36
4502	N	LYS	A	694	49.301	21.803	26.426	1.00	22.37
4503	CA	LYS	A	694	49.397	22.197	27.836	1.00	26.78
4504	C	LYS	A	694	48.227	23.020	28.342	1.00	25.75
4505	O	LYS	A	694	47.839	22.882	29.508	1.00	26.28
4506	CB	LYS	A	694	50.739	22.873	28.133	1.00	30.68
4507	CG	LYS	A	694	50.740	24.392	28.225	1.00	35.67
4508	CD	LYS	A	694	52.036	24.960	28.789	1.00	39.09
4509	CE	LYS	A	694	52.086	26.494	28.763	1.00	41.48

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4510	NZ	LYS	A	694	50.861	27.195	29.329	1.00	43.73
4511	N	THR	A	695	47.560	23.824	27.511	1.00	23.27
4512	CA	THR	A	695	46.427	24.609	27.898	1.00	24.00
4513	C	THR	A	695	45.076	23.936	27.789	1.00	21.80
4514	O	THR	A	695	44.094	24.597	28.158	1.00	23.18
4515	CB	THR	A	695	46.289	25.932	27.057	1.00	26.17
4516	OG1	THR	A	695	45.835	25.571	25.738	1.00	30.11
4517	CG2	THR	A	695	47.536	26.727	27.038	1.00	26.32
4518	N	ALA	A	696	44.970	22.725	27.246	1.00	17.97
4519	CA	ALA	A	696	43.659	22.141	27.079	1.00	19.04
4520	C	ALA	A	696	43.034	21.799	28.438	1.00	18.20
4521	O	ALA	A	696	43.750	21.502	29.404	1.00	17.08
4522	CB	ALA	A	696	43.747	20.900	26.195	1.00	18.12
4523	N	GLN	A	697	41.724	21.764	28.480	1.00	17.77
4524	CA	GLN	A	697	40.935	21.340	29.647	1.00	18.85
4525	C	GLN	A	697	40.214	20.039	29.320	1.00	19.35
4526	O	GLN	A	697	40.134	19.653	28.146	1.00	18.13
4527	CB	GLN	A	697	39.886	22.400	30.046	1.00	21.26
4528	CG	GLN	A	697	40.464	23.763	30.408	1.00	21.40
4529	CD	GLN	A	697	39.454	24.837	30.803	1.00	23.53
4530	OE1	GLN	A	697	39.895	25.823	31.487	1.00	25.32
4531	NE2	GLN	A	697	38.206	24.668	30.518	1.00	20.87
4532	N	GLY	A	698	39.716	19.300	30.312	1.00	18.21
4533	CA	GLY	A	698	38.991	18.051	30.069	1.00	16.88
4534	C	GLY	A	698	37.739	17.973	30.988	1.00	18.11
4535	O	GLY	A	698	37.289	19.027	31.463	1.00	18.21
4536	N	PHE	A	699	37.184	16.788	31.222	1.00	16.37
4537	CA	PHE	A	699	35.989	16.611	32.032	1.00	18.23
4538	C	PHE	A	699	36.113	17.182	33.445	1.00	18.02
4539	O	PHE	A	699	35.197	17.864	33.906	1.00	16.59
4540	CB	PHE	A	699	35.608	15.121	32.107	1.00	17.98
4541	CG	PHE	A	699	34.419	14.751	32.963	1.00	18.86
4542	CD1	PHE	A	699	34.594	14.201	34.229	1.00	17.66
4543	CD2	PHE	A	699	33.124	14.931	32.494	1.00	17.36
4544	CE1	PHE	A	699	33.481	13.856	35.006	1.00	18.49
4545	CE2	PHE	A	699	32.021	14.589	33.261	1.00	19.78
4546	CZ	PHE	A	699	32.189	14.044	34.525	1.00	19.39
4547	N	ALA	A	700	37.233	16.927	34.136	1.00	16.55
4548	CA	ALA	A	700	37.367	17.425	35.495	1.00	16.01
4549	C	ALA	A	700	37.613	18.922	35.560	1.00	17.98
4550	O	ALA	A	700	37.438	19.479	36.654	1.00	16.39
4551	CB	ALA	A	700	38.547	16.728	36.197	1.00	15.97
4552	N	THR	A	701	38.066	19.547	34.474	1.00	17.35
4553	CA	THR	A	701	38.531	20.920	34.525	1.00	18.55
4554	C	THR	A	701	37.744	21.889	33.629	1.00	19.85
4555	O	THR	A	701	38.226	23.004	33.458	1.00	20.14
4556	CB	THR	A	701	40.027	21.044	34.148	1.00	18.45
4557	OG1	THR	A	701	40.289	20.404	32.895	1.00	18.96
4558	CG2	THR	A	701	40.941	20.438	35.213	1.00	19.17
4559	N	GLY	A	702	36.558	21.526	33.166	1.00	21.54
4560	CA	GLY	A	702	35.692	22.478	32.466	1.00	23.96
4561	C	GLY	A	702	35.279	22.206	31.039	1.00	24.73
4562	O	GLY	A	702	34.407	22.929	30.527	1.00	23.67
4563	N	ASP	A	703	35.873	21.237	30.342	1.00	23.12
4564	CA	ASP	A	703	35.398	20.922	28.991	1.00	23.82
4565	C	ASP	A	703	34.070	20.187	29.093	1.00	23.19
4566	O	ASP	A	703	33.960	19.175	29.779	1.00	18.58
4567	CB	ASP	A	703	36.431	20.071	28.241	1.00	23.36
4568	CG	ASP	A	703	36.033	19.782	26.797	1.00	24.04
4569	OD1	ASP	A	703	36.618	20.476	25.930	1.00	25.71
4570	OD2	ASP	A	703	35.188	18.926	26.500	1.00	21.20
4571	N	PRO	A	704	33.059	20.609	28.324	1.00	24.11
4572	CA	PRO	A	704	31.731	20.018	28.400	1.00	23.04
4573	C	PRO	A	704	31.480	18.888	27.446	1.00	21.55
4574	O	PRO	A	704	30.401	18.265	27.492	1.00	21.23
4575	CB	PRO	A	704	30.809	21.220	28.065	1.00	24.82
4576	CG	PRO	A	704	31.633	21.977	27.058	1.00	25.35
4577	CD	PRO	A	704	33.080	21.823	27.468	1.00	24.45
4578	N	ASN	A	705	32.447	18.525	26.606	1.00	19.72
4579	CA	ASN	A	705	32.185	17.446	25.629	1.00	21.46
4580	C	ASN	A	705	32.802	16.090	25.927	1.00	23.27
4581	O	ASN	A	705	32.884	15.294	24.976	1.00	23.47
4582	CB	ASN	A	705	32.745	17.969	24.290	1.00	21.14
4583	CG	ASN	A	705	32.042	19.276	23.915	1.00	23.28
4584	OD1	ASN	A	705	30.818	19.366	24.062	1.00	23.01
4585	ND2	ASN	A	705	32.790	20.256	23.491	1.00	24.52
4586	N	GLN	A	706	33.030	15.688	27.187	1.00	21.97
4587	CA	GLN	A	706	33.650	14.375	27.459	1.00	21.06
4588	C	GLN	A	706	32.804	13.352	28.193	1.00	21.75
4589	O	GLN	A	706	33.297	12.317	28.660	1.00	20.03
4590	CB	GLN	A	706	34.918	14.683	28.310	1.00	20.55
4591	CG	GLN	A	706	35.854	15.729	27.750	1.00	19.45
4592	CD	GLN	A	706	36.345	15.354	26.363	1.00	23.83
4593	OE1	GLN	A	706	36.610	14.155	26.140	1.00	24.34
4594	NE2	GLN	A	706	36.463	16.280	25.413	1.00	22.80
4595	N	VAL	A	707	31.486	13.514	28.358	1.00	20.98
4596	CA	VAL	A	707	30.608	12.590	29.043	1.00	21.61
4597	C	VAL	A	707	30.703	11.153	28.513	1.00	23.14
4598	O	VAL	A	707	30.863	10.217	29.304	1.00	19.91
4599	CB	VAL	A	707	29.115	13.027	29.034	1.00	22.13
4600	CG1	VAL	A	707	28.133	11.953	29.488	1.00	18.96
4601	CG2	VAL	A	707	28.930	14.204	30.014	1.00	20.82
4602	N	ASP	A	708	30.635	10.964	27.180	1.00	23.14
4603	CA	ASP	A	708	30.701	9.604	26.647	1.00	22.35
4604	C	ASP	A	708	32.118	9.026	26.784	1.00	20.35
4605	O	ASP	A	708	32.175	7.813	26.913	1.00	18.36

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4606	CB	ASP	A	708	30.249	9.493	25.190	1.00	24.86
4607	CG	ASP	A	708	28.777	9.849	25.041	1.00	28.73
4608	OD1	ASP	A	708	27.911	9.562	25.888	1.00	29.20
4609	OD2	ASP	A	708	28.457	10.460	24.000	1.00	32.49
4610	N	VAL	A	709	33.177	9.833	26.732	1.00	19.19
4611	CA	VAL	A	709	34.512	9.243	26.985	1.00	19.71
4612	C	VAL	A	709	34.616	8.739	28.443	1.00	18.90
4613	O	VAL	A	709	35.086	7.622	28.734	1.00	16.65
4614	CB	VAL	A	709	35.604	10.248	26.676	1.00	19.27
4615	CG1	VAL	A	709	36.987	9.862	27.166	1.00	17.03
4616	CG2	VAL	A	709	35.640	10.467	25.138	1.00	21.90
4617	N	ILE	A	710	34.165	9.578	29.376	1.00	17.70
4618	CA	ILE	A	710	34.132	9.165	30.786	1.00	17.02
4619	C	ILE	A	710	33.319	7.907	30.995	1.00	16.46
4620	O	ILE	A	710	33.789	6.942	31.644	1.00	15.43
4621	CB	ILE	A	710	33.641	10.356	31.640	1.00	16.39
4622	CG1	ILE	A	710	34.615	11.533	31.483	1.00	19.18
4623	CG2	ILE	A	710	33.543	9.944	33.100	1.00	16.50
4624	CD1	ILE	A	710	36.090	11.238	31.712	1.00	15.64
4625	N	LYS	A	711	32.105	7.794	30.422	1.00	17.27
4626	CA	LYS	A	711	31.267	6.607	30.613	1.00	17.74
4627	C	LYS	A	711	31.972	5.347	30.102	1.00	17.56
4628	O	LYS	A	711	31.855	4.277	30.716	1.00	17.05
4629	CB	LYS	A	711	29.870	6.695	29.933	1.00	20.15
4630	CG	LYS	A	711	28.924	7.679	30.662	1.00	23.13
4631	CD	LYS	A	711	27.567	7.692	29.962	1.00	28.41
4632	CE	LYS	A	711	26.580	8.731	30.447	1.00	30.81
4633	NZ	LYS	A	711	25.271	8.572	29.682	1.00	34.74
4634	N	ASN	A	712	32.624	5.442	28.943	1.00	16.24
4635	CA	ASN	A	712	33.389	4.323	28.403	1.00	17.57
4636	C	ASN	A	712	34.537	3.949	29.358	1.00	16.07
4637	O	ASN	A	712	34.819	2.758	29.543	1.00	16.07
4638	CB	ASN	A	712	33.967	4.698	27.036	1.00	18.74
4639	CG	ASN	A	712	33.031	4.342	25.891	1.00	21.96
4640	OD1	ASN	A	712	32.812	3.181	25.595	1.00	21.32
4641	ND2	ASN	A	712	32.322	5.338	25.353	1.00	23.31
4642	N	GLY	A	713	35.160	4.910	30.029	1.00	15.84
4643	CA	GLY	A	713	36.196	4.574	31.026	1.00	15.68
4644	C	GLY	A	713	35.616	3.941	32.302	1.00	16.62
4645	O	GLY	A	713	36.235	3.026	32.905	1.00	15.22
4646	N	VAL	A	714	34.458	4.434	32.755	1.00	16.34
4647	CA	VAL	A	714	33.775	3.909	33.951	1.00	15.53
4648	C	VAL	A	714	33.490	2.430	33.793	1.00	15.76
4649	O	VAL	A	714	33.610	1.702	34.794	1.00	16.34
4650	CB	VAL	A	714	32.457	4.629	34.258	1.00	16.87
4651	CG1	VAL	A	714	31.474	3.887	35.168	1.00	14.77
4652	CG2	VAL	A	714	32.705	5.999	34.927	1.00	16.03
4653	N	ILE	A	715	33.060	1.928	32.632	1.00	16.13
4654	CA	ILE	A	715	32.769	0.468	32.556	1.00	15.59
4655	C	ILE	A	715	34.003	-0.389	32.207	1.00	16.37
4656	O	ILE	A	715	33.911	-1.557	31.784	1.00	14.09
4657	CB	ILE	A	715	31.619	0.207	31.554	1.00	15.72
4658	CG1	ILE	A	715	31.997	0.689	30.136	1.00	15.41
4659	CG2	ILE	A	715	30.315	0.959	31.967	1.00	15.73
4660	CD1	ILE	A	715	30.904	0.480	29.056	1.00	17.76
4661	N	GLY	A	716	35.234	0.099	32.413	1.00	15.99
4662	CA	GLY	A	716	36.440	-0.726	32.202	1.00	14.94
4663	C	GLY	A	716	36.808	-0.841	30.730	1.00	15.94
4664	O	GLY	A	716	37.424	-1.833	30.314	1.00	16.36
4665	N	SER	A	717	36.394	0.105	29.882	1.00	13.02
4666	CA	SER	A	717	36.785	0.122	28.471	1.00	15.05
4667	C	SER	A	717	36.284	-1.033	27.650	1.00	15.07
4668	O	SER	A	717	36.690	-1.154	26.479	1.00	15.88
4669	CB	SER	A	717	38.379	0.196	28.479	1.00	12.88
4670	OG	SER	A	717	38.624	1.550	28.854	1.00	16.45
4671	N	ILE	A	718	35.335	-1.833	28.140	1.00	13.58
4672	CA	ILE	A	718	34.833	-3.017	27.485	1.00	16.06
4673	C	ILE	A	718	34.018	-2.762	26.216	1.00	18.30
4674	O	ILE	A	718	33.755	-3.690	25.423	1.00	17.12
4675	CB	ILE	A	718	33.972	-3.868	28.463	1.00	14.85
4676	CG1	ILE	A	718	32.705	-3.102	28.902	1.00	14.22
4677	CG2	ILE	A	718	34.803	-4.358	29.641	1.00	13.95
4678	CD1	ILE	A	718	31.759	-3.997	29.708	1.00	14.94
4679	N	GLN	A	719	33.665	-1.511	25.966	1.00	20.52
4680	CA	GLN	A	719	33.070	-1.148	24.677	1.00	23.41
4681	C	GLN	A	719	34.019	-0.262	23.894	1.00	22.29
4682	O	GLN	A	719	33.605	0.413	22.972	1.00	21.69
4683	CB	GLN	A	719	31.726	-0.410	24.905	1.00	25.15
4684	CG	GLN	A	719	30.710	-1.398	25.487	1.00	29.75
4685	CD	GLN	A	719	30.193	-2.454	24.535	1.00	33.47
4686	OE1	GLN	A	719	30.552	-2.581	23.370	1.00	34.39
4687	NE2	GLN	A	719	29.279	-3.300	25.048	1.00	35.85
4688	N	ASP	A	720	35.274	-0.139	24.286	1.00	20.49
4689	CA	ASP	A	720	36.189	0.785	23.621	1.00	20.66
4690	C	ASP	A	720	37.361	-0.033	23.088	1.00	20.80
4691	O	ASP	A	720	37.521	-0.167	21.880	1.00	19.75
4692	CB	ASP	A	720	36.604	1.845	24.680	1.00	21.05
4693	CG	ASP	A	720	37.535	2.895	24.139	1.00	23.81
4694	OD1	ASP	A	720	37.824	2.819	22.920	1.00	23.07
4695	OD2	ASP	A	720	37.996	3.843	24.839	1.00	25.42
4696	N	PHE	A	721	38.162	-0.679	23.947	1.00	18.58
4697	CA	PHE	A	721	39.268	-1.508	23.422	1.00	18.29
4698	C	PHE	A	721	39.608	-2.722	24.262	1.00	19.42
4699	O	PHE	A	721	40.655	-3.321	23.961	1.00	18.82
4700	CB	PHE	A	721	40.557	-0.647	23.250	1.00	16.48
4701	CG	PHE	A	721	40.983	0.029	24.520	1.00	16.11

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4702	CD1	PHE	A	721	40.487	1.297	24.909	1.00	13.99
4703	CD2	PHE	A	721	41.893	-0.659	25.356	1.00	17.14
4704	CE1	PHE	A	721	40.966	1.833	26.081	1.00	14.66
4705	CE2	PHE	A	721	42.282	-0.123	26.610	1.00	15.32
4706	CZ	PHE	A	721	41.772	1.078	26.959	1.00	14.52
4707	N	THR	A	722	38.806	-3.129	25.271	1.00	18.35
4708	CA	THR	A	722	39.234	-4.301	26.048	1.00	18.71
4709	C	THR	A	722	38.256	-5.465	25.964	1.00	20.07
4710	O	THR	A	722	37.131	-5.187	25.605	1.00	15.87
4711	CB	THR	A	722	39.370	-4.000	27.568	1.00	18.02
4712	OG1	THR	A	722	38.074	-3.670	28.117	1.00	16.78
4713	CG2	THR	A	722	40.327	-2.847	27.866	1.00	14.81
4714	N	SER	A	723	38.634	-6.684	26.382	1.00	20.49
4715	CA	SER	A	723	37.652	-7.760	26.508	1.00	20.59
4716	C	SER	A	723	37.348	-8.047	27.978	1.00	19.48
4717	O	SER	A	723	36.524	-8.903	28.269	1.00	18.62
4718	CB	SER	A	723	38.180	-9.078	25.911	1.00	24.40
4719	OG	SER	A	723	38.237	-8.849	24.496	1.00	30.69
4720	N	ALA	A	724	38.066	-7.402	28.893	1.00	18.21
4721	CA	ALA	A	724	37.899	-7.608	30.343	1.00	19.12
4722	C	ALA	A	724	38.520	-6.384	31.027	1.00	17.24
4723	O	ALA	A	724	39.416	-5.778	30.461	1.00	14.91
4724	CB	ALA	A	724	38.614	-8.866	30.799	1.00	18.06
4725	N	PRO	A	725	38.026	-5.999	32.198	1.00	16.70
4726	CA	PRO	A	725	38.492	-4.783	32.855	1.00	16.71
4727	C	PRO	A	725	39.952	-4.840	33.276	1.00	15.43
4728	O	PRO	A	725	40.587	-3.775	33.366	1.00	14.10
4729	CB	PRO	A	725	37.489	-4.567	33.975	1.00	16.43
4730	CG	PRO	A	725	37.007	-5.964	34.298	1.00	16.92
4731	CD	PRO	A	725	36.921	-6.642	32.931	1.00	16.63
4732	N	SER	A	726	40.558	-6.013	33.429	1.00	14.30
4733	CA	SER	A	726	41.982	-6.146	33.752	1.00	16.27
4734	C	SER	A	726	42.918	-5.644	32.664	1.00	17.17
4735	O	SER	A	726	44.114	-5.417	32.923	1.00	16.54
4736	CB	SER	A	726	42.327	-7.619	34.067	1.00	15.36
4737	OG	SER	A	726	42.016	-8.458	32.938	1.00	16.05
4738	N	GLU	A	727	42.424	-5.385	31.443	1.00	17.23
4739	CA	GLU	A	727	43.285	-4.934	30.337	1.00	15.75
4740	C	GLU	A	727	43.407	-3.427	30.227	1.00	16.68
4741	O	GLU	A	727	44.127	-2.965	29.335	1.00	16.11
4742	CB	GLU	A	727	42.733	-5.464	29.003	1.00	16.78
4743	CG	GLU	A	727	42.684	-7.007	28.978	1.00	15.52
4744	CD	GLU	A	727	41.939	-7.565	27.761	1.00	17.00
4745	OE1	GLU	A	727	41.381	-6.829	26.934	1.00	15.44
4746	OE2	GLU	A	727	41.889	-8.794	27.542	1.00	17.47
4747	N	THR	A	728	42.758	-2.643	31.103	1.00	13.84
4748	CA	THR	A	728	42.902	-1.194	30.999	1.00	15.17
4749	C	THR	A	728	43.571	-0.687	32.286	1.00	15.61
4750	O	THR	A	728	43.030	-0.930	33.380	1.00	15.14
4751	CB	THR	A	728	41.587	-0.424	30.739	1.00	14.97
4752	OG1	THR	A	728	41.796	1.025	30.886	1.00	15.95
4753	CG2	THR	A	728	40.515	-0.764	31.802	1.00	14.40
4754	N	ILE	A	729	44.667	0.062	32.166	1.00	14.75
4755	CA	ILE	A	729	45.295	0.716	33.325	1.00	14.43
4756	C	ILE	A	729	44.727	2.155	33.337	1.00	15.83
4757	O	ILE	A	729	45.145	2.937	32.453	1.00	17.36
4758	CB	ILE	A	729	46.818	0.776	33.179	1.00	15.12
4759	CG1	ILE	A	729	47.417	-0.582	32.833	1.00	13.83
4760	CG2	ILE	A	729	47.496	1.228	34.524	1.00	16.20
4761	CD1	ILE	A	729	47.025	-1.766	33.724	1.00	11.75
4762	N	ASN	A	730	43.764	2.501	34.179	1.00	15.29
4763	CA	ASN	A	730	43.155	3.831	34.153	1.00	16.11
4764	C	ASN	A	730	44.036	4.865	34.850	1.00	15.71
4765	O	ASN	A	730	44.559	4.561	35.927	1.00	14.58
4766	CB	ASN	A	730	41.764	3.781	34.807	1.00	16.99
4767	CG	ASN	A	730	40.776	2.775	34.203	1.00	16.76
4768	OD1	ASN	A	730	39.932	2.076	34.846	1.00	17.80
4769	ND2	ASN	A	730	40.923	2.747	32.900	1.00	14.18
4770	N	TYR	A	731	44.303	6.022	34.261	1.00	14.78
4771	CA	TYR	A	731	45.135	7.013	34.912	1.00	16.43
4772	C	TYR	A	731	44.889	8.442	34.401	1.00	16.53
4773	O	TYR	A	731	44.321	8.554	33.309	1.00	16.09
4774	CB	TYR	A	731	46.641	6.738	34.752	1.00	16.77
4775	CG	TYR	A	731	47.189	6.951	33.358	1.00	17.72
4776	CD1	TYR	A	731	48.208	7.865	33.101	1.00	18.91
4777	CD2	TYR	A	731	46.723	6.190	32.306	1.00	16.97
4778	CE1	TYR	A	731	48.689	8.074	31.810	1.00	20.50
4779	CE2	TYR	A	731	47.152	6.393	31.015	1.00	19.21
4780	CZ	TYR	A	731	48.157	7.321	30.782	1.00	22.10
4781	OH	TYR	A	731	48.585	7.473	29.473	1.00	22.66
4782	N	VAL	A	732	45.463	9.396	35.150	1.00	14.45
4783	CA	VAL	A	732	45.429	10.782	34.652	1.00	15.94
4784	C	VAL	A	732	46.793	11.401	34.486	1.00	15.92
4785	O	VAL	A	732	46.949	12.340	33.663	1.00	16.20
4786	CB	VAL	A	732	44.507	11.667	35.541	1.00	16.99
4787	CG1	VAL	A	732	44.997	11.697	36.988	1.00	13.37
4788	CG2	VAL	A	732	44.444	13.123	35.006	1.00	17.23
4789	N	THR	A	733	47.822	11.034	35.242	1.00	15.69
4790	CA	THR	A	733	49.189	11.535	35.142	1.00	16.13
4791	C	THR	A	733	50.244	10.428	35.359	1.00	16.11
4792	O	THR	A	733	49.918	9.357	35.898	1.00	13.88
4793	CB	THR	A	733	49.597	12.657	36.115	1.00	17.42
4794	OG1	THR	A	733	49.438	12.231	37.477	1.00	15.92
4795	CG2	THR	A	733	48.827	13.958	35.888	1.00	14.57
4796	N	SER	A	734	51.504	10.693	34.974	1.00	16.76
4797	CA	SER	A	734	52.607	9.753	35.168	1.00	16.69

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4798	C	SER	A	734	53.925	10.520	35.190	1.00	17.73
4799	O	SER	A	734	53.869	11.751	35.123	1.00	18.37
4800	CB	SER	A	734	52.699	8.630	34.116	1.00	16.19
4801	OG	SER	A	734	53.031	9.220	32.839	1.00	17.55
4802	N	HIS	A	735	55.095	9.901	35.332	1.00	16.87
4803	CA	HIS	A	735	56.355	10.627	35.335	1.00	18.13
4804	C	HIS	A	735	56.582	11.454	34.067	1.00	18.58
4805	O	HIS	A	735	57.307	12.484	34.165	1.00	20.77
4806	CB	HIS	A	735	57.585	9.714	35.570	1.00	16.15
4807	CG	HIS	A	735	57.897	8.867	34.358	1.00	16.14
4808	ND1	HIS	A	735	57.309	7.621	34.171	1.00	13.70
4809	CD2	HIS	A	735	58.707	9.141	33.286	1.00	14.91
4810	CE1	HIS	A	735	57.772	7.135	33.010	1.00	16.16
4811	NE2	HIS	A	735	58.586	8.039	32.480	1.00	16.01
4812	N	ASP	A	736	56.069	11.050	32.912	1.00	18.06
4813	CA	ASP	A	736	56.221	11.847	31.698	1.00	18.55
4814	C	ASP	A	736	55.296	13.073	31.785	1.00	19.59
4815	O	ASP	A	736	54.252	13.058	32.472	1.00	14.38
4816	CB	ASP	A	736	55.851	11.014	30.458	1.00	19.05
4817	CG	ASP	A	736	56.916	10.045	29.971	1.00	19.36
4818	OD1	ASP	A	736	58.079	10.474	29.782	1.00	18.46
4819	OD2	ASP	A	736	56.639	8.828	29.769	1.00	19.23
4820	N	ASN	A	737	55.648	14.149	31.055	1.00	19.40
4821	CA	ASN	A	737	54.827	15.353	31.031	1.00	19.79
4822	C	ASN	A	737	54.651	15.987	32.411	1.00	20.31
4823	O	ASN	A	737	55.545	15.914	33.270	1.00	18.64
4824	CB	ASN	A	737	53.499	15.028	30.295	1.00	20.11
4825	CG	ASN	A	737	53.794	14.336	28.972	1.00	23.21
4826	OD1	ASN	A	737	53.500	13.160	28.760	1.00	23.28
4827	ND2	ASN	A	737	54.473	14.985	28.022	1.00	23.64
4828	N	MET	A	738	53.530	16.651	32.711	1.00	19.26
4829	CA	MET	A	738	53.389	17.416	33.938	1.00	19.59
4830	C	MET	A	738	52.657	16.709	35.085	1.00	19.41
4831	O	MET	A	738	51.854	15.813	34.846	1.00	17.92
4832	CB	MET	A	738	52.619	18.711	33.619	1.00	20.83
4833	CG	MET	A	738	53.300	19.598	32.561	1.00	22.68
4834	SD	MET	A	738	52.260	21.070	32.188	1.00	25.13
4835	CE	MET	A	738	52.683	22.154	33.456	1.00	22.07
4836	N	THR	A	739	52.939	17.124	36.311	1.00	17.76
4837	CA	THR	A	739	52.155	16.614	37.447	1.00	18.00
4838	C	THR	A	739	50.770	17.275	37.332	1.00	18.02
4839	O	THR	A	739	50.609	18.312	36.672	1.00	18.06
4840	CB	THR	A	739	52.781	16.952	38.809	1.00	19.29
4841	OG1	THR	A	739	52.642	18.358	39.103	1.00	17.62
4842	CG2	THR	A	739	54.267	16.607	38.889	1.00	17.97
4843	N	LEU	A	740	49.739	16.694	37.916	1.00	16.11
4844	CA	LEU	A	740	48.403	17.232	37.843	1.00	17.22
4845	C	LEU	A	740	48.315	18.636	38.430	1.00	16.52
4846	O	LEU	A	740	47.642	19.447	37.769	1.00	17.44
4847	CB	LEU	A	740	47.300	16.323	38.417	1.00	15.94
4848	CG	LEU	A	740	45.862	16.743	38.020	1.00	16.72
4849	CD1	LEU	A	740	45.757	16.769	36.484	1.00	16.81
4850	CD2	LEU	A	740	44.836	15.720	38.527	1.00	14.02
4851	N	TRP	A	741	48.917	18.934	39.557	1.00	16.04
4852	CA	TRP	A	741	48.920	20.276	40.119	1.00	18.09
4853	C	TRP	A	741	49.452	21.316	39.117	1.00	20.12
4854	O	TRP	A	741	48.838	22.376	38.903	1.00	20.13
4855	CB	TRP	A	741	49.692	20.303	41.435	1.00	17.80
4856	CG	TRP	A	741	49.450	21.549	42.242	1.00	18.78
4857	CD1	TRP	A	741	50.376	22.463	42.644	1.00	20.16
4858	CD2	TRP	A	741	48.169	22.020	42.713	1.00	18.03
4859	NE1	TRP	A	741	49.758	23.472	43.361	1.00	21.18
4860	CE2	TRP	A	741	48.395	23.219	43.395	1.00	20.56
4861	CE3	TRP	A	741	46.866	21.539	42.591	1.00	17.60
4862	CZ2	TRP	A	741	47.368	23.961	44.000	1.00	20.50
4863	CZ3	TRP	A	741	45.827	22.277	43.159	1.00	17.86
4864	CH2	TRP	A	741	46.083	23.467	43.857	1.00	19.81
4865	N	ASP	A	742	50.582	21.019	38.485	1.00	19.17
4866	CA	ASP	A	742	51.203	21.880	37.484	1.00	19.35
4867	C	ASP	A	742	50.350	21.984	36.222	1.00	17.93
4868	O	ASP	A	742	50.146	23.081	35.724	1.00	16.62
4869	CB	ASP	A	742	52.592	21.376	37.082	1.00	18.32
4870	CG	ASP	A	742	53.612	21.544	38.183	1.00	18.67
4871	OD1	ASP	A	742	53.279	21.975	39.300	1.00	19.97
4872	OD2	ASP	A	742	54.794	21.167	38.023	1.00	18.27
4873	N	LYS	A	743	49.809	20.860	35.768	1.00	19.25
4874	CA	LYS	A	743	48.930	20.830	34.597	1.00	20.46
4875	C	LYS	A	743	47.680	21.685	34.812	1.00	20.53
4876	O	LYS	A	743	47.388	22.506	33.953	1.00	18.46
4877	CB	LYS	A	743	48.540	19.395	34.234	1.00	19.12
4878	CG	LYS	A	743	47.336	19.231	33.334	1.00	18.93
4879	CD	LYS	A	743	47.578	19.872	31.951	1.00	20.19
4880	CE	LYS	A	743	46.198	20.097	31.314	1.00	18.13
4881	NZ	LYS	A	743	46.312	20.465	29.867	1.00	16.42
4882	N	ILE	A	744	47.000	21.537	35.966	1.00	20.06
4883	CA	ILE	A	744	45.812	22.353	36.210	1.00	19.39
4884	C	ILE	A	744	46.150	23.835	36.365	1.00	20.80
4885	O	ILE	A	744	45.365	24.660	35.853	1.00	22.66
4886	CB	ILE	A	744	44.977	21.824	37.385	1.00	20.28
4887	CG1	ILE	A	744	44.363	20.462	36.995	1.00	17.01
4888	CG2	ILE	A	744	43.850	22.807	37.780	1.00	18.88
4889	CD1	ILE	A	744	43.768	19.712	38.182	1.00	15.17
4890	N	LEU	A	745	47.292	24.254	36.899	1.00	19.68
4891	CA	LEU	A	745	47.690	25.652	36.898	1.00	23.49
4892	C	LEU	A	745	47.839	26.228	35.465	1.00	24.82
4893	O	LEU	A	745	47.471	27.398	35.201	1.00	23.41

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4894	CB	LEU	A	745	49.072	25.836	37.539	1.00	24.77
4895	CG	LEU	A	745	49.509	27.212	37.976	1.00	28.42
4896	CD1	LEU	A	745	48.531	27.865	38.985	1.00	28.65
4897	CD2	LEU	A	745	50.857	27.244	38.702	1.00	29.02
4898	N	ALA	A	746	48.322	25.358	34.544	1.00	22.10
4899	CA	ALA	A	746	48.486	25.844	33.172	1.00	21.79
4900	C	ALA	A	746	47.184	25.938	32.398	1.00	21.61
4901	O	ALA	A	746	47.055	26.813	31.530	1.00	21.69
4902	CB	ALA	A	746	49.458	24.871	32.456	1.00	19.18
4903	N	SER	A	747	46.292	24.932	32.552	1.00	19.68
4904	CA	SER	A	747	45.040	24.968	31.851	1.00	19.92
4905	C	SER	A	747	44.016	25.873	32.565	1.00	20.35
4906	O	SER	A	747	43.053	26.199	31.881	1.00	19.89
4907	CB	SER	A	747	44.372	23.594	31.621	1.00	19.80
4908	OG	SER	A	747	44.018	22.968	32.866	1.00	22.16
4909	N	ASN	A	748	44.061	26.141	33.871	1.00	20.37
4910	CA	ASN	A	748	42.972	26.892	34.557	1.00	20.69
4911	C	ASN	A	748	43.616	27.982	35.418	1.00	21.19
4912	O	ASN	A	748	43.508	28.025	36.658	1.00	22.97
4913	CB	ASN	A	748	42.230	25.944	35.499	1.00	20.68
4914	CG	ASN	A	748	41.301	24.953	34.831	1.00	21.99
4915	OD1	ASN	A	748	40.043	25.156	34.923	1.00	24.93
4916	ND2	ASN	A	748	41.827	23.973	34.134	1.00	18.77
4917	N	PRO	A	749	44.412	28.851	34.819	1.00	22.66
4918	CA	PRO	A	749	45.192	29.825	35.564	1.00	24.77
4919	C	PRO	A	749	44.317	30.787	36.354	1.00	24.99
4920	O	PRO	A	749	44.780	31.208	37.413	1.00	28.37
4921	CB	PRO	A	749	46.076	30.507	34.506	1.00	23.57
4922	CG	PRO	A	749	45.240	30.423	33.269	1.00	25.06
4923	CD	PRO	A	749	44.574	29.067	33.359	1.00	22.65
4924	N	SER	A	750	43.100	31.111	35.973	1.00	27.45
4925	CA	SER	A	750	42.373	32.079	36.834	1.00	30.33
4926	C	SER	A	750	41.454	31.439	37.876	1.00	30.12
4927	O	SER	A	750	40.824	32.153	38.673	1.00	28.54
4928	CB	SER	A	750	41.708	33.101	35.932	1.00	30.51
4929	OG	SER	A	750	40.743	32.469	35.086	1.00	33.66
4930	N	ASP	A	751	41.410	30.106	37.977	1.00	27.22
4931	CA	ASP	A	751	40.591	29.469	39.011	1.00	25.49
4932	C	ASP	A	751	41.317	29.534	40.356	1.00	23.90
4933	O	ASP	A	751	42.551	29.566	40.384	1.00	21.81
4934	CB	ASP	A	751	40.251	28.035	38.640	1.00	25.71
4935	CG	ASP	A	751	39.119	27.964	37.643	1.00	27.68
4936	OD1	ASP	A	751	38.017	28.510	37.899	1.00	29.06
4937	OD2	ASP	A	751	39.317	27.350	36.581	1.00	27.19
4938	N	THR	A	752	40.546	29.584	41.463	1.00	21.83
4939	CA	THR	A	752	41.159	29.653	42.779	1.00	20.72
4940	C	THR	A	752	41.855	28.311	43.098	1.00	21.26
4941	O	THR	A	752	41.582	27.259	42.500	1.00	19.88
4942	CB	THR	A	752	40.151	29.916	43.915	1.00	20.18
4943	OG1	THR	A	752	39.251	28.794	44.021	1.00	16.86
4944	CG2	THR	A	752	39.235	31.142	43.708	1.00	18.66
4945	N	GLU	A	753	42.751	28.429	44.076	1.00	21.78
4946	CA	GLU	A	753	43.429	27.308	44.672	1.00	23.03
4947	C	GLU	A	753	42.430	26.254	45.153	1.00	21.75
4948	O	GLU	A	753	42.616	25.067	44.834	1.00	19.13
4949	CB	GLU	A	753	44.332	27.648	45.874	1.00	24.56
4950	CG	GLU	A	753	45.287	26.501	46.181	1.00	28.93
4951	CD	GLU	A	753	46.304	26.813	47.238	1.00	33.40
4952	OE1	GLU	A	753	47.067	25.968	47.729	1.00	35.28
4953	OE2	GLU	A	753	46.378	28.035	47.614	1.00	34.78
4954	N	ALA	A	754	41.408	26.715	45.929	1.00	19.55
4955	CA	ALA	A	754	40.439	25.748	46.423	1.00	18.95
4956	C	ALA	A	754	39.776	25.048	45.242	1.00	18.59
4957	O	ALA	A	754	39.434	23.831	45.331	1.00	16.89
4958	CB	ALA	A	754	39.358	26.388	47.347	1.00	17.73
4959	N	ASP	A	755	39.310	25.765	44.207	1.00	18.37
4960	CA	ASP	A	755	38.675	25.066	43.077	1.00	17.43
4961	C	ASP	A	755	39.646	24.137	42.339	1.00	18.14
4962	O	ASP	A	755	39.290	23.031	41.834	1.00	18.30
4963	CB	ASP	A	755	38.025	26.070	42.112	1.00	19.81
4964	CG	ASP	A	755	36.624	26.560	42.475	1.00	21.04
4965	OD1	ASP	A	755	36.190	27.580	41.939	1.00	21.93
4966	OD2	ASP	A	755	35.899	25.957	43.290	1.00	21.94
4967	N	ARG	A	756	40.914	24.503	42.188	1.00	18.10
4968	CA	ARG	A	756	41.891	23.655	41.478	1.00	16.46
4969	C	ARG	A	756	42.146	22.409	42.341	1.00	16.36
4970	O	ARG	A	756	42.201	21.306	41.780	1.00	14.27
4971	CB	ARG	A	756	43.168	24.439	41.108	1.00	17.08
4972	CG	ARG	A	756	42.898	25.555	40.071	1.00	20.15
4973	CD	ARG	A	756	44.176	26.286	39.593	1.00	21.05
4974	NE	ARG	A	756	44.608	27.330	40.496	1.00	22.58
4975	CZ	ARG	A	756	45.623	27.329	41.346	1.00	22.14
4976	NH1	ARG	A	756	46.474	26.353	41.521	1.00	22.42
4977	NH2	ARG	A	756	45.814	28.363	42.142	1.00	24.17
4978	N	ILE	A	757	42.144	22.500	43.688	1.00	15.45
4979	CA	ILE	A	757	42.170	21.297	44.521	1.00	15.56
4980	C	ILE	A	757	40.977	20.388	44.257	1.00	16.59
4981	O	ILE	A	757	41.151	19.162	43.993	1.00	16.56
4982	CB	ILE	A	757	42.316	21.636	46.034	1.00	17.09
4983	CG1	ILE	A	757	43.755	22.055	46.341	1.00	15.23
4984	CG2	ILE	A	757	41.894	20.412	46.892	1.00	16.32
4985	CD1	ILE	A	757	44.008	22.725	47.668	1.00	16.53
4986	N	LYS	A	758	39.751	20.951	44.189	1.00	15.17
4987	CA	LYS	A	758	38.587	20.110	43.886	1.00	17.48
4988	C	LYS	A	758	38.686	19.381	42.557	1.00	16.06
4989	O	LYS	A	758	38.285	18.211	42.451	1.00	15.89

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4990	CB	LYS	A	758	37.245	20.915	43.892	1.00	15.97
4991	CG	LYS	A	758	36.909	21.285	45.349	1.00	18.80
4992	CD	LYS	A	758	35.437	21.596	45.583	1.00	19.89
4993	CE	LYS	A	758	35.018	22.900	44.976	1.00	21.56
4994	NZ	LYS	A	758	33.521	22.969	44.892	1.00	23.65
4995	N	MET	A	759	39.199	20.079	41.536	1.00	15.74
4996	CA	MET	A	759	39.327	19.517	40.200	1.00	15.98
4997	C	MET	A	759	40.354	18.390	40.160	1.00	14.93
4998	O	MET	A	759	40.113	17.359	39.550	1.00	16.46
4999	CB	MET	A	759	39.733	20.623	39.208	1.00	17.07
5000	CG	MET	A	759	38.714	21.707	38.855	1.00	19.35
5001	SD	MET	A	759	39.471	23.010	37.839	1.00	19.26
5002	CE	MET	A	759	38.242	24.312	37.984	1.00	21.66
5003	N	ASP	A	760	41.459	18.508	40.908	1.00	16.22
5004	CA	ASP	A	760	42.480	17.450	41.007	1.00	16.26
5005	C	ASP	A	760	41.911	16.200	41.659	1.00	17.21
5006	O	ASP	A	760	42.042	15.049	41.214	1.00	17.75
5007	CB	ASP	A	760	43.645	18.034	41.819	1.00	17.31
5008	CG	ASP	A	760	44.913	17.214	41.946	1.00	17.03
5009	OD1	ASP	A	760	44.793	15.983	42.065	1.00	15.47
5010	OD2	ASP	A	760	46.047	17.756	41.909	1.00	14.89
5011	N	GLU	A	761	41.234	16.368	42.799	1.00	16.56
5012	CA	GLU	A	761	40.568	15.332	43.536	1.00	16.85
5013	C	GLU	A	761	39.469	14.695	42.670	1.00	16.63
5014	O	GLU	A	761	39.350	13.466	42.667	1.00	15.05
5015	CB	GLU	A	761	39.959	15.955	44.815	1.00	18.53
5016	CG	GLU	A	761	40.986	16.290	45.884	1.00	17.58
5017	CD	GLU	A	761	40.366	16.960	47.100	1.00	18.11
5018	OE1	GLU	A	761	41.075	16.978	48.131	1.00	18.18
5019	OE2	GLU	A	761	39.202	17.438	47.086	1.00	15.48
5020	N	LEU	A	762	38.681	15.476	41.908	1.00	14.32
5021	CA	LEU	A	762	37.725	14.847	40.991	1.00	15.45
5022	C	LEU	A	762	38.352	13.989	39.897	1.00	13.62
5023	O	LEU	A	762	37.806	12.922	39.595	1.00	13.44
5024	CB	LEU	A	762	36.841	15.905	40.308	1.00	16.49
5025	CG	LEU	A	762	35.804	15.442	39.294	1.00	20.45
5026	CD1	LEU	A	762	34.763	14.500	39.907	1.00	18.27
5027	CD2	LEU	A	762	35.059	16.623	38.651	1.00	20.38
5028	N	ALA	A	763	39.439	14.449	39.244	1.00	13.62
5029	CA	ALA	A	763	40.002	13.575	38.205	1.00	14.02
5030	C	ALA	A	763	40.440	12.248	38.843	1.00	13.98
5031	O	ALA	A	763	40.245	11.182	38.264	1.00	14.29
5032	CB	ALA	A	763	41.186	14.252	37.523	1.00	15.43
5033	N	HIS	A	764	41.107	12.268	39.991	1.00	13.75
5034	CA	HIS	A	764	41.529	11.018	40.633	1.00	14.85
5035	C	HIS	A	764	40.340	10.203	41.116	1.00	15.09
5036	O	HIS	A	764	40.318	8.959	41.071	1.00	14.64
5037	CB	HIS	A	764	42.523	11.373	41.764	1.00	16.48
5038	CG	HIS	A	764	43.881	11.820	41.290	1.00	16.16
5039	ND1	HIS	A	764	44.861	10.897	40.931	1.00	17.78
5040	CD2	HIS	A	764	44.425	13.045	41.106	1.00	14.29
5041	CE1	HIS	A	764	45.980	11.539	40.576	1.00	13.10
5042	NE2	HIS	A	764	45.734	12.822	40.663	1.00	18.06
5043	N	ALA	A	765	39.263	10.853	41.598	1.00	14.85
5044	CA	ALA	A	765	38.050	10.167	42.039	1.00	15.19
5045	C	ALA	A	765	37.481	9.281	40.923	1.00	15.79
5046	O	ALA	A	765	36.976	8.170	41.144	1.00	15.86
5047	CB	ALA	A	765	36.973	11.185	42.490	1.00	15.09
5048	N	VAL	A	766	37.426	9.768	39.691	1.00	15.11
5049	CA	VAL	A	766	37.011	8.984	38.524	1.00	14.49
5050	C	VAL	A	766	37.969	7.801	38.348	1.00	15.68
5051	O	VAL	A	766	37.484	6.669	38.206	1.00	15.59
5052	CB	VAL	A	766	36.967	9.813	37.215	1.00	14.83
5053	CG1	VAL	A	766	36.639	8.953	35.976	1.00	13.21
5054	CG2	VAL	A	766	35.898	10.921	37.371	1.00	13.49
5055	N	VAL	A	767	39.295	8.026	38.448	1.00	15.32
5056	CA	VAL	A	767	40.182	6.831	38.337	1.00	15.78
5057	C	VAL	A	767	39.874	5.778	39.405	1.00	16.72
5058	O	VAL	A	767	39.783	4.553	39.099	1.00	16.35
5059	CB	VAL	A	767	41.656	7.260	38.475	1.00	15.24
5060	CG1	VAL	A	767	42.610	6.067	38.588	1.00	13.41
5061	CG2	VAL	A	767	42.126	8.151	37.317	1.00	14.80
5062	N	PHE	A	768	39.717	6.221	40.658	1.00	16.27
5063	CA	PHE	A	768	39.471	5.305	41.772	1.00	16.07
5064	C	PHE	A	768	38.094	4.659	41.812	1.00	16.53
5065	O	PHE	A	768	37.996	3.555	42.413	1.00	15.80
5066	CB	PHE	A	768	39.838	5.868	43.137	1.00	15.94
5067	CG	PHE	A	768	41.238	6.460	43.307	1.00	16.54
5068	CD1	PHE	A	768	41.402	7.676	43.923	1.00	15.00
5069	CD2	PHE	A	768	42.374	5.808	42.882	1.00	17.09
5070	CE1	PHE	A	768	42.654	8.258	44.120	1.00	16.04
5071	CE2	PHE	A	768	43.640	6.366	43.042	1.00	17.04
5072	CZ	PHE	A	768	43.783	7.583	43.673	1.00	16.63
5073	N	THR	A	769	37.041	5.156	41.149	1.00	15.47
5074	CA	THR	A	769	35.736	4.475	41.230	1.00	14.36
5075	C	THR	A	769	35.328	3.823	39.920	1.00	15.61
5076	O	THR	A	769	34.198	3.269	39.801	1.00	15.87
5077	CB	THR	A	769	34.620	5.443	41.691	1.00	15.41
5078	OG1	THR	A	769	34.713	6.617	40.902	1.00	14.96
5079	CG2	THR	A	769	34.762	5.855	43.174	1.00	15.33
5080	N	SER	A	770	36.220	3.901	38.906	1.00	14.01
5081	CA	SER	A	770	35.921	3.261	37.631	1.00	14.16
5082	C	SER	A	770	36.302	1.788	37.682	1.00	14.69
5083	O	SER	A	770	37.326	1.408	38.247	1.00	13.64
5084	CB	SER	A	770	36.746	3.878	36.481	1.00	14.15
5085	OG	SER	A	770	36.278	5.140	36.080	1.00	11.78

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5086	N	GLN	A	771	35.626	0.960	36.880	1.00	13.77
5087	CA	GLN	A	771	36.006	-0.422	36.664	1.00	13.99
5088	C	GLN	A	771	37.356	-0.464	35.925	1.00	15.46
5089	O	GLN	A	771	37.647	0.442	35.136	1.00	12.49
5090	CB	GLN	A	771	34.970	-1.223	35.849	1.00	13.53
5091	CG	GLN	A	771	33.544	-1.161	36.443	1.00	13.08
5092	CD	GLN	A	771	33.426	-1.789	37.822	1.00	14.69
5093	OE1	GLN	A	771	32.830	-1.185	38.752	1.00	17.76
5094	NE2	GLN	A	771	33.956	-2.976	38.040	1.00	10.21
5095	N	GLY	A	772	38.232	-1.456	36.210	1.00	15.16
5096	CA	GLY	A	772	39.559	-1.446	35.598	1.00	14.97
5097	C	GLY	A	772	40.698	-1.432	36.635	1.00	17.39
5098	O	GLY	A	772	40.444	-1.663	37.829	1.00	17.47
5099	N	VAL	A	773	41.944	-1.109	36.210	1.00	14.33
5100	CA	VAL	A	773	43.079	-1.067	37.150	1.00	14.45
5101	C	VAL	A	773	43.498	0.376	37.463	1.00	14.94
5102	O	VAL	A	773	44.084	0.998	36.611	1.00	16.35
5103	CB	VAL	A	773	44.310	-1.795	36.560	1.00	13.88
5104	CG1	VAL	A	773	45.422	-1.889	37.632	1.00	14.66
5105	CG2	VAL	A	773	44.005	-3.217	36.086	1.00	12.67
5106	N	PRO	A	774	43.257	0.966	38.599	1.00	13.58
5107	CA	PRO	A	774	43.649	2.341	38.928	1.00	15.84
5108	C	PRO	A	774	45.167	2.545	39.130	1.00	15.75
5109	O	PRO	A	774	45.813	1.748	39.817	1.00	15.14
5110	CB	PRO	A	774	42.834	2.611	40.199	1.00	14.18
5111	CG	PRO	A	774	42.710	1.231	40.899	1.00	14.41
5112	CD	PRO	A	774	42.527	0.274	39.729	1.00	13.83
5113	N	PHE	A	775	45.788	3.610	38.635	1.00	14.44
5114	CA	PHE	A	775	47.223	3.894	38.687	1.00	13.52
5115	C	PHE	A	775	47.368	5.379	39.009	1.00	15.10
5116	O	PHE	A	775	46.501	6.130	38.554	1.00	13.30
5117	CB	PHE	A	775	47.900	3.601	37.345	1.00	12.64
5118	CG	PHE	A	775	49.278	4.170	37.094	1.00	13.05
5119	CD1	PHE	A	775	49.496	5.505	36.842	1.00	12.94
5120	CD2	PHE	A	775	50.356	3.300	37.074	1.00	14.88
5121	CE1	PHE	A	775	50.749	6.040	36.616	1.00	15.54
5122	CE2	PHE	A	775	51.633	3.813	36.809	1.00	16.38
5123	CZ	PHE	A	775	51.828	5.157	36.592	1.00	15.45
5124	N	MET	A	776	48.332	5.763	39.836	1.00	14.40
5125	CA	MET	A	776	48.537	7.192	40.097	1.00	15.32
5126	C	MET	A	776	50.042	7.492	40.068	1.00	16.66
5127	O	MET	A	776	50.796	6.561	40.340	1.00	16.26
5128	CB	MET	A	776	47.999	7.642	41.453	1.00	14.34
5129	CG	MET	A	776	48.432	6.833	42.653	1.00	15.93
5130	SD	MET	A	776	47.677	7.342	44.233	1.00	13.48
5131	CE	MET	A	776	48.304	9.017	44.325	1.00	14.69
5132	N	GLN	A	777	50.420	8.732	39.804	1.00	16.06
5133	CA	GLN	A	777	51.838	9.108	39.931	1.00	15.06
5134	C	GLN	A	777	52.082	9.345	41.420	1.00	13.74
5135	O	GLN	A	777	51.281	10.097	41.996	1.00	12.00
5136	CB	GLN	A	777	52.175	10.388	39.136	1.00	15.88
5137	CG	GLN	A	777	53.660	10.809	39.318	1.00	14.21
5138	CD	GLN	A	777	54.081	12.028	38.491	1.00	16.72
5139	OE1	GLN	A	777	55.294	12.354	38.396	1.00	15.28
5140	NE2	GLN	A	777	53.132	12.777	37.931	1.00	13.34
5141	N	GLY	A	778	53.109	8.770	42.037	1.00	14.51
5142	CA	GLY	A	778	53.354	8.968	43.469	1.00	12.51
5143	C	GLY	A	778	53.552	10.434	43.782	1.00	15.81
5144	O	GLY	A	778	54.236	11.120	42.976	1.00	16.75
5145	N	GLY	A	779	52.939	10.912	44.890	1.00	14.32
5146	CA	GLY	A	779	53.108	12.345	45.197	1.00	14.20
5147	C	GLY	A	779	51.919	13.204	44.778	1.00	13.35
5148	O	GLY	A	779	51.774	14.341	45.263	1.00	13.40
5149	N	GLU	A	780	51.027	12.713	43.910	1.00	12.45
5150	CA	GLU	A	780	49.829	13.482	43.533	1.00	12.05
5151	C	GLU	A	780	48.913	13.718	44.746	1.00	14.09
5152	O	GLU	A	780	48.336	14.808	44.855	1.00	15.37
5153	CB	GLU	A	780	48.989	12.898	42.410	1.00	13.91
5154	CG	GLU	A	780	49.577	12.770	41.025	1.00	16.76
5155	CD	GLU	A	780	50.238	13.981	40.396	1.00	20.75
5156	OE1	GLU	A	780	51.146	14.633	41.024	1.00	19.70
5157	OE2	GLU	A	780	49.891	14.243	39.214	1.00	19.72
5158	N	GLU	A	781	48.866	12.843	45.725	1.00	14.52
5159	CA	GLU	A	781	48.154	12.941	46.974	1.00	15.90
5160	C	GLU	A	781	48.654	14.108	47.829	1.00	18.04
5161	O	GLU	A	781	47.923	14.505	48.739	1.00	16.36
5162	CB	GLU	A	781	48.261	11.644	47.797	1.00	15.13
5163	CG	GLU	A	781	49.627	11.402	48.399	1.00	16.08
5164	CD	GLU	A	781	50.695	10.808	47.504	1.00	16.18
5165	OE1	GLU	A	781	51.749	10.429	48.068	1.00	16.29
5166	OE2	GLU	A	781	50.534	10.719	46.283	1.00	13.64
5167	N	MET	A	782	49.842	14.681	47.552	1.00	18.10
5168	CA	MET	A	782	50.278	15.860	48.278	1.00	18.57
5169	C	MET	A	782	50.588	17.012	47.311	1.00	18.29
5170	O	MET	A	782	51.393	17.853	47.652	1.00	19.99
5171	CB	MET	A	782	51.460	15.657	49.216	1.00	19.24
5172	CG	MET	A	782	52.667	14.956	48.626	1.00	21.00
5173	SD	MET	A	782	53.939	14.548	49.843	1.00	19.47
5174	CE	MET	A	782	55.206	13.871	48.770	1.00	24.22
5175	N	LEU	A	783	49.947	17.109	46.165	1.00	17.38
5176	CA	LEU	A	783	50.155	18.163	45.193	1.00	18.72
5177	C	LEU	A	783	51.620	18.346	44.767	1.00	19.18
5178	O	LEU	A	783	52.145	19.459	44.641	1.00	18.25
5179	CB	LEU	A	783	49.475	19.451	45.699	1.00	17.56
5180	CG	LEU	A	783	48.014	19.300	46.199	1.00	17.76
5181	CD1	LEU	A	783	47.488	20.670	46.671	1.00	17.88

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5182	CD2	LEU	A	783	47.044	18.790	45.147	1.00	17.03
5183	N	ARG	A	784	52.365	17.273	44.548	1.00	18.59
5184	CA	ARG	A	784	53.781	17.338	44.128	1.00	16.30
5185	C	ARG	A	784	53.899	18.310	42.947	1.00	16.06
5186	O	ARG	A	784	53.105	18.204	42.016	1.00	13.00
5187	CB	ARG	A	784	54.303	15.965	43.754	1.00	16.36
5188	CG	ARG	A	784	55.732	15.937	43.128	1.00	15.05
5189	CD	ARG	A	784	56.414	14.612	43.471	1.00	14.37
5190	NE	ARG	A	784	57.508	14.212	42.581	1.00	15.11
5191	CZ	ARG	A	784	57.463	13.745	41.344	1.00	15.39
5192	NH1	ARG	A	784	56.328	13.510	40.649	1.00	14.22
5193	NH2	ARG	A	784	58.620	13.430	40.733	1.00	14.18
5194	N	THR	A	785	54.889	19.199	42.961	1.00	16.44
5195	CA	THR	A	785	55.115	20.158	41.892	1.00	15.86
5196	C	THR	A	785	56.506	20.037	41.278	1.00	17.13
5197	O	THR	A	785	57.501	19.843	41.965	1.00	17.03
5198	CB	THR	A	785	54.867	21.626	42.325	1.00	16.69
5199	OG1	THR	A	785	55.174	22.534	41.239	1.00	15.16
5200	CG2	THR	A	785	55.649	22.074	43.552	1.00	17.25
5201	N	LYS	A	786	56.614	20.188	39.958	1.00	18.17
5202	CA	LYS	A	786	57.921	20.173	39.294	1.00	17.98
5203	C	LYS	A	786	58.229	21.610	38.838	1.00	19.45
5204	O	LYS	A	786	59.132	21.831	38.027	1.00	18.14
5205	CB	LYS	A	786	57.889	19.233	38.073	1.00	16.77
5206	CG	LYS	A	786	57.954	17.750	38.423	1.00	14.96
5207	CD	LYS	A	786	57.859	16.802	37.187	1.00	14.97
5208	CE	LYS	A	786	57.877	15.352	37.713	1.00	15.19
5209	NZ	LYS	A	786	57.719	14.341	36.641	1.00	16.24
5210	N	GLY	A	787	57.436	22.583	39.295	1.00	18.49
5211	CA	GLY	A	787	57.644	23.974	38.910	1.00	20.70
5212	C	GLY	A	787	57.258	24.206	37.454	1.00	22.88
5213	O	GLY	A	787	57.860	25.094	36.818	1.00	23.87
5214	N	GLY	A	788	56.399	23.347	36.861	1.00	21.35
5215	CA	GLY	A	788	56.109	23.489	35.452	1.00	21.36
5216	C	GLY	A	788	56.890	22.565	34.521	1.00	22.43
5217	O	GLY	A	788	56.521	22.424	33.344	1.00	22.35
5218	N	ASN	A	789	57.981	21.941	34.970	1.00	21.38
5219	CA	ASN	A	789	58.756	21.085	34.057	1.00	20.82
5220	C	ASN	A	789	57.880	20.009	33.441	1.00	22.07
5221	O	ASN	A	789	57.169	19.288	34.156	1.00	21.85
5222	CB	ASN	A	789	59.929	20.450	34.788	1.00	21.40
5223	CG	ASN	A	789	61.082	20.034	33.891	1.00	21.99
5224	OD1	ASN	A	789	62.224	20.457	34.093	1.00	23.49
5225	ND2	ASN	A	789	60.832	19.188	32.936	1.00	19.50
5226	N	ASP	A	790	57.941	19.850	32.117	1.00	21.23
5227	CA	ASP	A	790	57.167	18.811	31.470	1.00	22.38
5228	C	ASP	A	790	57.988	17.637	30.939	1.00	20.63
5229	O	ASP	A	790	57.393	16.915	30.142	1.00	19.94
5230	CB	ASP	A	790	56.287	19.374	30.343	1.00	26.38
5231	CG	ASP	A	790	57.068	19.930	29.177	1.00	30.47
5232	OD1	ASP	A	790	56.515	20.793	28.455	1.00	33.68
5233	OD2	ASP	A	790	58.222	19.566	28.904	1.00	31.34
5234	N	ASN	A	791	59.253	17.444	31.250	1.00	19.26
5235	CA	ASN	A	791	60.065	16.323	30.796	1.00	20.27
5236	C	ASN	A	791	61.345	16.285	31.637	1.00	21.29
5237	O	ASN	A	791	62.427	16.809	31.319	1.00	21.30
5238	CB	ASN	A	791	60.399	16.462	29.302	1.00	21.32
5239	CG	ASN	A	791	61.287	15.363	28.764	1.00	23.30
5240	OD1	ASN	A	791	62.204	15.598	27.948	1.00	22.34
5241	ND2	ASN	A	791	60.989	14.150	29.217	1.00	20.57
5242	N	SER	A	792	61.156	15.862	32.889	1.00	18.66
5243	CA	SER	A	792	62.048	15.872	34.014	1.00	18.76
5244	C	SER	A	792	63.218	14.927	34.077	1.00	17.02
5245	O	SER	A	792	63.795	14.823	35.171	1.00	15.69
5246	CB	SER	A	792	61.153	15.277	35.222	1.00	21.30
5247	OG	SER	A	792	60.809	16.404	35.929	1.00	26.39
5248	N	TYR	A	793	63.515	14.156	33.037	1.00	17.61
5249	CA	TYR	A	793	64.461	13.062	33.084	1.00	19.03
5250	C	TYR	A	793	65.842	13.343	33.677	1.00	19.80
5251	O	TYR	A	793	66.409	12.383	34.224	1.00	19.27
5252	CB	TYR	A	793	64.553	12.429	31.682	1.00	22.02
5253	CG	TYR	A	793	65.461	13.221	30.737	1.00	23.77
5254	CD1	TYR	A	793	66.790	12.827	30.544	1.00	23.83
5255	CD2	TYR	A	793	64.965	14.342	30.075	1.00	22.77
5256	CE1	TYR	A	793	67.610	13.552	29.690	1.00	24.44
5257	CE2	TYR	A	793	65.776	15.058	29.210	1.00	24.72
5258	CZ	TYR	A	793	67.098	14.657	29.040	1.00	24.81
5259	OH	TYR	A	793	67.896	15.388	28.191	1.00	26.96
5260	N	ASN	A	794	66.476	14.496	33.547	1.00	19.42
5261	CA	ASN	A	794	67.801	14.743	34.132	1.00	22.06
5262	C	ASN	A	794	67.762	16.039	34.931	1.00	22.30
5263	O	ASN	A	794	68.798	16.678	35.115	1.00	21.57
5264	CB	ASN	A	794	68.903	14.841	33.039	1.00	22.69
5265	CG	ASN	A	794	68.772	16.021	32.093	1.00	25.22
5266	OD1	ASN	A	794	67.764	16.759	32.048	1.00	24.93
5267	ND2	ASN	A	794	69.779	16.287	31.241	1.00	25.15
5268	N	ALA	A	795	66.562	16.450	35.392	1.00	22.67
5269	CA	ALA	A	795	66.383	17.734	36.035	1.00	21.37
5270	C	ALA	A	795	66.819	17.900	37.481	1.00	20.96
5271	O	ALA	A	795	66.796	19.075	37.914	1.00	20.75
5272	CB	ALA	A	795	64.896	18.177	35.919	1.00	19.65
5273	N	GLY	A	796	67.107	16.854	38.225	1.00	18.52
5274	CA	GLY	A	796	67.646	17.021	39.556	1.00	19.89
5275	C	GLY	A	796	66.566	16.955	40.632	1.00	19.49
5276	O	GLY	A	796	65.390	16.814	40.294	1.00	18.74
5277	N	ASP	A	797	66.989	17.117	41.871	1.00	18.66

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5278	CA	ASP	A	797	66.128	16.903	43.044	1.00	20.03
5279	C	ASP	A	797	65.167	18.013	43.367	1.00	21.02
5280	O	ASP	A	797	63.994	17.803	43.701	1.00	20.32
5281	CB	ASP	A	797	67.067	16.594	44.244	1.00	19.80
5282	CG	ASP	A	797	68.007	15.440	44.019	1.00	19.46
5283	OD1	ASP	A	797	69.230	15.521	44.326	1.00	21.24
5284	OD2	ASP	A	797	67.633	14.351	43.526	1.00	20.79
5285	N	SER	A	798	65.560	19.280	43.210	1.00	21.85
5286	CA	SER	A	798	64.685	20.423	43.474	1.00	24.03
5287	C	SER	A	798	63.395	20.374	42.665	1.00	22.30
5288	O	SER	A	798	62.323	20.682	43.172	1.00	19.63
5289	CB	SER	A	798	65.451	21.739	43.216	1.00	27.04
5290	OG	SER	A	798	64.488	22.790	43.346	1.00	33.22
5291	N	VAL	A	799	63.473	19.840	41.450	1.00	19.85
5292	CA	VAL	A	799	62.354	19.588	40.579	1.00	19.39
5293	C	VAL	A	799	61.603	18.281	40.867	1.00	19.66
5294	O	VAL	A	799	60.379	18.346	40.925	1.00	18.31
5295	CB	VAL	A	799	62.837	19.448	39.110	1.00	19.45
5296	CG1	VAL	A	799	61.707	19.105	38.147	1.00	17.83
5297	CG2	VAL	A	799	63.547	20.738	38.692	1.00	20.77
5298	N	ASN	A	800	62.310	17.147	40.988	1.00	18.33
5299	CA	ASN	A	800	61.651	15.856	41.130	1.00	17.55
5300	C	ASN	A	800	61.376	15.299	42.514	1.00	16.34
5301	O	ASN	A	800	60.637	14.312	42.626	1.00	15.95
5302	CB	ASN	A	800	62.512	14.802	40.393	1.00	17.74
5303	CG	ASN	A	800	62.543	14.987	38.883	1.00	19.36
5304	OD1	ASN	A	800	63.584	15.273	38.249	1.00	20.67
5305	ND2	ASN	A	800	61.404	14.856	38.247	1.00	17.72
5306	N	GLN	A	801	61.969	15.783	43.590	1.00	14.69
5307	CA	GLN	A	801	61.866	15.102	44.861	1.00	18.63
5308	C	GLN	A	801	60.471	15.071	45.487	1.00	16.56
5309	O	GLN	A	801	59.644	15.874	45.101	1.00	15.25
5310	CB	GLN	A	801	62.806	15.707	45.932	1.00	17.66
5311	CG	GLN	A	801	62.342	17.090	46.382	1.00	19.69
5312	CD	GLN	A	801	63.483	17.927	46.966	1.00	21.59
5313	OE1	GLN	A	801	64.500	17.414	47.435	1.00	22.85
5314	NE2	GLN	A	801	63.304	19.240	47.068	1.00	21.07
5315	N	PHE	A	802	60.305	14.158	46.429	1.00	16.13
5316	CA	PHE	A	802	59.071	14.118	47.240	1.00	18.33
5317	C	PHE	A	802	59.323	15.192	48.327	1.00	18.45
5318	O	PHE	A	802	60.112	14.942	49.246	1.00	19.38
5319	CB	PHE	A	802	58.763	12.759	47.875	1.00	16.57
5320	CG	PHE	A	802	58.053	11.737	47.006	1.00	19.68
5321	CD1	PHE	A	802	58.287	11.656	45.645	1.00	18.62
5322	CD2	PHE	A	802	57.109	10.859	47.565	1.00	20.70
5323	CE1	PHE	A	802	57.590	10.747	44.860	1.00	20.67
5324	CE2	PHE	A	802	56.413	9.938	46.778	1.00	20.96
5325	CZ	PHE	A	802	56.693	9.865	45.429	1.00	19.43
5326	N	ASP	A	803	58.624	16.288	48.253	1.00	18.57
5327	CA	ASP	A	803	58.808	17.357	49.254	1.00	19.86
5328	C	ASP	A	803	57.793	17.081	50.357	1.00	20.28
5329	O	ASP	A	803	56.641	17.492	50.205	1.00	19.15
5330	CB	ASP	A	803	58.610	18.731	48.651	1.00	22.65
5331	CG	ASP	A	803	58.669	19.930	49.590	1.00	25.08
5332	OD1	ASP	A	803	58.806	19.685	50.814	1.00	25.27
5333	OD2	ASP	A	803	58.588	21.104	49.167	1.00	23.70
5334	N	TRP	A	804	58.233	16.380	51.405	1.00	18.05
5335	CA	TRP	A	804	57.319	15.921	52.445	1.00	19.41
5336	C	TRP	A	804	56.629	16.989	53.289	1.00	21.10
5337	O	TRP	A	804	55.653	16.669	53.993	1.00	19.44
5338	CB	TRP	A	804	57.946	14.789	53.243	1.00	18.06
5339	CG	TRP	A	804	58.290	13.537	52.497	1.00	19.31
5340	CD1	TRP	A	804	59.477	13.263	51.863	1.00	18.88
5341	CD2	TRP	A	804	57.474	12.380	52.297	1.00	19.81
5342	NE1	TRP	A	804	59.448	12.034	51.283	1.00	18.40
5343	CE2	TRP	A	804	58.216	11.461	51.531	1.00	18.59
5344	CE3	TRP	A	804	56.163	12.061	52.677	1.00	18.95
5345	CZ2	TRP	A	804	57.722	10.222	51.155	1.00	17.95
5346	CZ3	TRP	A	804	55.674	10.809	52.304	1.00	18.76
5347	CH2	TRP	A	804	56.437	9.922	51.551	1.00	17.47
5348	N	SER	A	805	57.047	18.260	53.210	1.00	21.38
5349	CA	SER	A	805	56.412	19.375	53.886	1.00	21.85
5350	C	SER	A	805	55.047	19.592	53.219	1.00	21.71
5351	O	SER	A	805	54.135	20.065	53.884	1.00	23.61
5352	CB	SER	A	805	57.197	20.695	53.829	1.00	19.87
5353	OG	SER	A	805	57.187	21.301	52.527	1.00	19.02
5354	N	ARG	A	806	54.822	19.172	51.974	1.00	19.88
5355	CA	ARG	A	806	53.512	19.335	51.351	1.00	22.24
5356	C	ARG	A	806	52.442	18.396	51.883	1.00	21.51
5357	O	ARG	A	806	51.254	18.722	51.750	1.00	19.94
5358	CB	ARG	A	806	53.636	19.156	49.822	1.00	24.11
5359	CG	ARG	A	806	54.034	20.543	49.260	1.00	26.24
5360	CD	ARG	A	806	54.401	20.399	47.801	1.00	24.25
5361	NE	ARG	A	806	53.327	20.788	46.893	1.00	21.27
5362	CZ	ARG	A	806	53.057	22.032	46.574	1.00	20.40
5363	NH1	ARG	A	806	53.779	23.031	47.094	1.00	21.72
5364	NH2	ARG	A	806	52.132	22.253	45.677	1.00	18.36
5365	N	LYS	A	807	52.841	17.251	52.437	1.00	20.38
5366	CA	LYS	A	807	51.865	16.365	53.068	1.00	20.37
5367	C	LYS	A	807	51.298	17.082	54.296	1.00	21.65
5368	O	LYS	A	807	50.107	17.019	54.552	1.00	21.63
5369	CB	LYS	A	807	52.501	15.007	53.414	1.00	17.10
5370	CG	LYS	A	807	51.504	14.093	54.081	1.00	18.69
5371	CD	LYS	A	807	52.030	12.677	54.344	1.00	16.56
5372	CE	LYS	A	807	50.960	11.883	55.134	1.00	15.71
5373	NZ	LYS	A	807	51.497	10.512	55.378	1.00	14.68

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5374	N	ALA	A	808	52.112	17.787	55.077	1.00	20.44
5375	CA	ALA	A	808	51.606	18.577	56.202	1.00	23.20
5376	C	ALA	A	808	50.732	19.752	55.729	1.00	22.93
5377	O	ALA	A	808	49.629	19.995	56.222	1.00	22.27
5378	CB	ALA	A	808	52.751	19.163	57.024	1.00	21.77
5379	N	GLN	A	809	51.188	20.477	54.706	1.00	23.92
5380	CA	GLN	A	809	50.492	21.617	54.146	1.00	23.89
5381	C	GLN	A	809	49.162	21.215	53.507	1.00	23.43
5382	O	GLN	A	809	48.168	21.944	53.608	1.00	20.37
5383	CB	GLN	A	809	51.356	22.355	53.095	1.00	25.14
5384	CG	GLN	A	809	50.627	23.521	52.421	1.00	26.75
5385	CD	GLN	A	809	51.547	24.361	51.551	1.00	29.36
5386	OE1	GLN	A	809	52.735	24.031	51.422	1.00	28.08
5387	NE2	GLN	A	809	51.050	25.449	50.941	1.00	30.28
5388	N	PHE	A	810	49.159	20.078	52.774	1.00	22.26
5389	CA	PHE	A	810	47.883	19.685	52.166	1.00	21.21
5390	C	PHE	A	810	47.375	18.387	52.769	1.00	21.19
5391	O	PHE	A	810	46.913	17.517	52.055	1.00	20.62
5392	CB	PHE	A	810	47.972	19.699	50.628	1.00	21.55
5393	CG	PHE	A	810	48.291	21.048	50.004	1.00	21.38
5394	CD1	PHE	A	810	49.557	21.281	49.481	1.00	20.93
5395	CD2	PHE	A	810	47.348	22.067	49.928	1.00	21.54
5396	CE1	PHE	A	810	49.832	22.549	48.923	1.00	22.85
5397	CE2	PHE	A	810	47.627	23.285	49.368	1.00	21.34
5398	CZ	PHE	A	810	48.881	23.543	48.856	1.00	22.67
5399	N	LYS	A	811	47.406	18.195	54.087	1.00	21.74
5400	CA	LYS	A	811	46.912	16.982	54.753	1.00	21.92
5401	C	LYS	A	811	45.455	16.673	54.422	1.00	21.36
5402	O	LYS	A	811	45.136	15.481	54.277	1.00	17.59
5403	CB	LYS	A	811	47.062	17.024	56.289	1.00	23.82
5404	CG	LYS	A	811	46.896	15.669	56.992	1.00	25.05
5405	CD	LYS	A	811	47.863	14.620	56.452	1.00	27.06
5406	CE	LYS	A	811	48.035	13.364	57.285	1.00	27.83
5407	NZ	LYS	A	811	46.792	12.947	57.977	1.00	30.70
5408	N	ASP	A	812	44.587	17.696	54.229	1.00	20.57
5409	CA	ASP	A	812	43.212	17.388	53.835	1.00	21.91
5410	C	ASP	A	812	43.149	16.742	52.456	1.00	20.65
5411	O	ASP	A	812	42.273	15.900	52.246	1.00	18.27
5412	CB	ASP	A	812	42.210	18.549	53.848	1.00	24.59
5413	CG	ASP	A	812	42.003	19.147	55.221	1.00	28.89
5414	OD1	ASP	A	812	41.473	20.283	55.328	1.00	31.55
5415	OD2	ASP	A	812	42.371	18.534	56.241	1.00	28.92
5416	N	VAL	A	813	44.036	17.111	51.539	1.00	18.77
5417	CA	VAL	A	813	44.040	16.444	50.227	1.00	18.35
5418	C	VAL	A	813	44.516	15.007	50.355	1.00	16.42
5419	O	VAL	A	813	43.987	14.074	49.741	1.00	16.64
5420	CB	VAL	A	813	44.922	17.275	49.264	1.00	19.35
5421	CG1	VAL	A	813	44.998	16.618	47.885	1.00	16.35
5422	CG2	VAL	A	813	44.486	18.742	49.166	1.00	19.07
5423	N	PHE	A	814	45.548	14.793	51.166	1.00	16.24
5424	CA	PHE	A	814	46.057	13.444	51.406	1.00	16.82
5425	C	PHE	A	814	44.943	12.573	51.982	1.00	17.46
5426	O	PHE	A	814	44.795	11.422	51.542	1.00	17.98
5427	CB	PHE	A	814	47.209	13.524	52.431	1.00	16.63
5428	CG	PHE	A	814	47.862	12.187	52.659	1.00	16.39
5429	CD1	PHE	A	814	49.038	11.891	51.984	1.00	16.20
5430	CD2	PHE	A	814	47.296	11.269	53.540	1.00	16.49
5431	CE1	PHE	A	814	49.633	10.652	52.204	1.00	17.12
5432	CE2	PHE	A	814	47.896	10.030	53.752	1.00	18.46
5433	CZ	PHE	A	814	49.062	9.746	53.077	1.00	18.20
5434	N	ASP	A	815	44.207	13.085	52.974	1.00	15.05
5435	CA	ASP	A	815	43.133	12.307	53.595	1.00	17.46
5436	C	ASP	A	815	42.017	11.960	52.607	1.00	16.89
5437	O	ASP	A	815	41.334	10.919	52.706	1.00	19.94
5438	CB	ASP	A	815	42.555	13.118	54.789	1.00	17.34
5439	CG	ASP	A	815	43.531	13.119	55.974	1.00	20.48
5440	OD1	ASP	A	815	44.579	12.408	55.987	1.00	19.52
5441	OD2	ASP	A	815	43.252	13.962	56.862	1.00	21.01
5442	N	TYR	A	816	41.683	12.885	51.710	1.00	16.33
5443	CA	TYR	A	816	40.663	12.564	50.678	1.00	16.00
5444	C	TYR	A	816	41.171	11.496	49.742	1.00	15.70
5445	O	TYR	A	816	40.397	10.580	49.417	1.00	16.79
5446	CB	TYR	A	816	40.309	13.837	49.869	1.00	16.36
5447	CG	TYR	A	816	39.217	13.680	48.824	1.00	15.25
5448	CD1	TYR	A	816	39.444	13.129	47.564	1.00	15.93
5449	CD2	TYR	A	816	37.918	14.077	49.117	1.00	15.92
5450	CE1	TYR	A	816	38.400	12.970	46.633	1.00	15.05
5451	CE2	TYR	A	816	36.886	13.958	48.209	1.00	16.61
5452	CZ	TYR	A	816	37.111	13.358	46.984	1.00	17.64
5453	OH	TYR	A	816	36.060	13.227	46.088	1.00	19.15
5454	N	PHE	A	817	42.434	11.487	49.320	1.00	12.51
5455	CA	PHE	A	817	42.962	10.474	48.436	1.00	13.42
5456	C	PHE	A	817	42.911	9.109	49.162	1.00	13.97
5457	O	PHE	A	817	42.435	8.133	48.606	1.00	13.72
5458	CB	PHE	A	817	44.389	10.643	47.942	1.00	13.63
5459	CG	PHE	A	817	44.578	11.514	46.713	1.00	12.99
5460	CD1	PHE	A	817	45.189	10.988	45.577	1.00	14.35
5461	CD2	PHE	A	817	44.228	12.837	46.732	1.00	14.28
5462	CE1	PHE	A	817	45.442	11.773	44.444	1.00	14.16
5463	CE2	PHE	A	817	44.474	13.644	45.615	1.00	15.25
5464	CZ	PHE	A	817	45.056	13.124	44.486	1.00	14.04
5465	N	SER	A	818	43.376	9.113	50.407	1.00	12.87
5466	CA	SER	A	818	43.354	7.917	51.238	1.00	15.48
5467	C	SER	A	818	41.955	7.389	51.512	1.00	14.72
5468	O	SER	A	818	41.744	6.162	51.485	1.00	16.73
5469	CB	SER	A	818	44.054	8.289	52.573	1.00	17.81

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5470	OG	SER A 818	43.841	7.176	53.431	1.00	22.91
5471	N	SER A 819	40.963	8.251	51.745	1.00	15.04
5472	CA	SER A 819	39.598	7.723	51.978	1.00	17.08
5473	C	SER A 819	39.014	7.080	50.731	1.00	15.58
5474	O	SER A 819	38.311	6.062	50.828	1.00	15.56
5475	CB	SER A 819	38.630	8.852	52.401	1.00	18.73
5476	OG	SER A 819	39.098	9.381	53.642	1.00	18.88
5477	N	MET A 820	39.241	7.652	49.551	1.00	16.10
5478	CA	MET A 820	38.739	7.072	48.304	1.00	18.56
5479	C	MET A 820	39.374	5.710	48.019	1.00	18.57
5480	O	MET A 820	38.727	4.747	47.598	1.00	16.01
5481	CB	MET A 820	39.001	8.018	47.123	1.00	20.82
5482	CG	MET A 820	38.153	7.749	45.900	1.00	23.16
5483	SD	MET A 820	36.405	8.041	45.961	1.00	22.93
5484	CE	MET A 820	36.118	9.783	45.834	1.00	23.13
5485	N	ILE A 821	40.688	5.642	48.244	1.00	17.40
5486	CA	ILE A 821	41.451	4.412	48.042	1.00	16.52
5487	C	ILE A 821	41.001	3.334	49.035	1.00	16.03
5488	O	ILE A 821	40.730	2.223	48.588	1.00	14.41
5489	CB	ILE A 821	42.975	4.656	48.056	1.00	15.70
5490	CG1	ILE A 821	43.474	5.516	46.885	1.00	13.40
5491	CG2	ILE A 821	43.644	3.255	48.054	1.00	15.43
5492	CD1	ILE A 821	44.782	6.262	47.154	1.00	11.03
5493	N	HIS A 822	40.778	3.678	50.314	1.00	14.76
5494	CA	HIS A 822	40.300	2.633	51.237	1.00	16.65
5495	C	HIS A 822	38.874	2.147	50.890	1.00	18.07
5496	O	HIS A 822	38.504	0.977	51.044	1.00	16.15
5497	CB	HIS A 822	40.389	3.195	52.667	1.00	18.28
5498	CG	HIS A 822	41.797	3.237	53.209	1.00	18.71
5499	ND1	HIS A 822	42.240	2.252	54.074	1.00	22.35
5500	CD2	HIS A 822	42.825	4.101	53.055	1.00	17.41
5501	CE1	HIS A 822	43.525	2.504	54.403	1.00	19.56
5502	NE2	HIS A 822	43.884	3.652	53.816	1.00	20.90
5503	N	LEU A 823	38.009	3.101	50.498	1.00	14.46
5504	CA	LEU A 823	36.670	2.802	50.021	1.00	15.73
5505	C	LEU A 823	36.756	1.864	48.847	1.00	15.38
5506	O	LEU A 823	36.209	0.707	49.030	1.00	15.40
5507	CB	LEU A 823	35.882	4.028	49.576	1.00	19.45
5508	CG	LEU A 823	34.486	3.700	49.019	1.00	21.92
5509	CD1	LEU A 823	33.474	3.712	50.151	1.00	25.56
5510	CD2	LEU A 823	34.106	4.685	47.925	1.00	25.24
5511	N	ARG A 824	37.475	2.025	47.744	1.00	14.25
5512	CA	ARG A 824	37.617	0.995	46.740	1.00	13.61
5513	C	ARG A 824	38.197	-0.307	47.284	1.00	14.10
5514	O	ARG A 824	37.659	-1.363	46.894	1.00	15.81
5515	CB	ARG A 824	38.584	1.423	45.592	1.00	13.50
5516	CG	ARG A 824	38.612	0.463	44.411	1.00	12.90
5517	CD	ARG A 824	39.803	0.839	43.450	1.00	14.06
5518	NE	ARG A 824	39.853	-0.095	42.310	1.00	12.64
5519	CZ	ARG A 824	39.049	-0.024	41.238	1.00	14.31
5520	NH1	ARG A 824	38.127	0.944	41.136	1.00	13.55
5521	NH2	ARG A 824	39.174	-0.928	40.254	1.00	14.66
5522	N	ASN A 825	39.145	-0.268	48.232	1.00	14.31
5523	CA	ASN A 825	39.689	-1.523	48.760	1.00	16.54
5524	C	ASN A 825	38.644	-2.390	49.496	1.00	15.73
5525	O	ASN A 825	38.693	-3.608	49.448	1.00	12.95
5526	CB	ASN A 825	40.877	-1.380	49.720	1.00	14.70
5527	CG	ASN A 825	42.129	-0.771	49.136	1.00	17.12
5528	OD1	ASN A 825	42.988	-0.200	49.853	1.00	19.07
5529	ND2	ASN A 825	42.310	-0.737	47.823	1.00	13.10
5530	N	GLN A 826	37.741	-1.663	50.181	1.00	18.02
5531	CA	GLN A 826	36.695	-2.358	50.934	1.00	20.90
5532	C	GLN A 826	35.477	-2.876	50.182	1.00	20.36
5533	O	GLN A 826	34.651	-3.630	50.742	1.00	19.69
5534	CB	GLN A 826	36.132	-1.381	51.993	1.00	26.32
5535	CG	GLN A 826	36.580	-1.691	53.397	1.00	35.56
5536	CD	GLN A 826	36.182	-3.094	53.844	1.00	39.06
5537	OE1	GLN A 826	35.589	-3.891	53.119	1.00	42.26
5538	NE2	GLN A 826	36.412	-3.345	55.128	1.00	41.91
5539	N	HIS A 827	35.234	-2.404	48.976	1.00	16.91
5540	CA	HIS A 827	34.036	-2.689	48.202	1.00	16.78
5541	C	HIS A 827	34.350	-3.273	46.840	1.00	15.74
5542	O	HIS A 827	34.555	-2.536	45.872	1.00	13.89
5543	CB	HIS A 827	33.257	-1.326	48.096	1.00	15.20
5544	CG	HIS A 827	32.617	-0.988	49.413	1.00	16.26
5545	ND1	HIS A 827	33.202	-0.101	50.300	1.00	20.12
5546	CD2	HIS A 827	31.489	-1.420	50.032	1.00	14.76
5547	CE1	HIS A 827	32.440	0.011	51.389	1.00	16.71
5548	NE2	HIS A 827	31.427	-0.829	51.254	1.00	19.08
5549	N	PRO A 828	34.325	-4.608	46.724	1.00	15.11
5550	CA	PRO A 828	34.560	-5.321	45.497	1.00	14.14
5551	C	PRO A 828	33.561	-5.010	44.393	1.00	15.45
5552	O	PRO A 828	33.881	-5.329	43.255	1.00	15.72
5553	CB	PRO A 828	34.468	-6.783	45.898	1.00	16.09
5554	CG	PRO A 828	33.621	-6.815	47.163	1.00	14.98
5555	CD	PRO A 828	34.044	-5.548	47.851	1.00	14.73
5556	N	ALA A 829	32.423	-4.314	44.652	1.00	14.28
5557	CA	ALA A 829	31.572	-3.851	43.558	1.00	14.18
5558	C	ALA A 829	32.312	-2.961	42.554	1.00	15.27
5559	O	ALA A 829	31.927	-2.910	41.374	1.00	14.49
5560	CB	ALA A 829	30.396	-3.007	44.068	1.00	10.50
5561	N	PHE A 830	33.342	-2.252	43.022	1.00	15.95
5562	CA	PHE A 830	34.152	-1.385	42.170	1.00	16.15
5563	C	PHE A 830	35.195	-2.117	41.342	1.00	16.91
5564	O	PHE A 830	35.922	-1.562	40.474	1.00	15.96
5565	CB	PHE A 830	34.922	-0.393	43.124	1.00	17.49

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5566	CG	PHE	A	830	33.982	0.683	43.674	1.00	18.77
5567	CD1	PHE	A	830	33.498	1.663	42.823	1.00	17.67
5568	CD2	PHE	A	830	33.671	0.733	45.029	1.00	19.33
5569	CE1	PHE	A	830	32.667	2.668	43.352	1.00	18.46
5570	CE2	PHE	A	830	32.777	1.688	45.534	1.00	18.20
5571	CZ	PHE	A	830	32.304	2.663	44.685	1.00	18.78
5572	N	ARG	A	831	35.349	-3.406	41.627	1.00	15.44
5573	CA	ARG	A	831	36.378	-4.252	41.039	1.00	16.14
5574	C	ARG	A	831	35.894	-5.556	40.438	1.00	16.54
5575	O	ARG	A	831	36.425	-6.657	40.688	1.00	16.91
5576	CB	ARG	A	831	37.362	-4.574	42.188	1.00	16.96
5577	CG	ARG	A	831	38.080	-3.419	42.858	1.00	16.46
5578	CD	ARG	A	831	38.971	-3.779	44.005	1.00	17.94
5579	NE	ARG	A	831	38.365	-3.942	45.328	1.00	17.80
5580	CZ	ARG	A	831	38.198	-5.082	45.971	1.00	18.41
5581	NH1	ARG	A	831	38.542	-6.244	45.421	1.00	18.63
5582	NH2	ARG	A	831	37.617	-5.115	47.169	1.00	18.47
5583	N	MET	A	832	34.819	-5.468	39.649	1.00	16.98
5584	CA	MET	A	832	34.280	-6.623	38.923	1.00	16.56
5585	C	MET	A	832	35.367	-7.141	37.961	1.00	17.92
5586	O	MET	A	832	36.184	-6.323	37.488	1.00	17.69
5587	CB	MET	A	832	33.002	-6.169	38.210	1.00	16.53
5588	CG	MET	A	832	31.834	-5.953	39.241	1.00	15.93
5589	SD	MET	A	832	30.273	-5.680	38.352	1.00	14.50
5590	CE	MET	A	832	30.215	-3.878	38.401	1.00	13.68
5591	N	THR	A	833	35.416	-8.440	37.714	1.00	16.30
5592	CA	THR	A	833	36.465	-8.992	36.872	1.00	17.66
5593	C	THR	A	833	36.119	-9.364	35.440	1.00	19.22
5594	O	THR	A	833	37.057	-9.531	34.621	1.00	17.30
5595	CB	THR	A	833	37.064	-10.227	37.580	1.00	17.12
5596	OG1	THR	A	833	36.053	-11.222	37.737	1.00	18.20
5597	CG2	THR	A	833	37.634	-9.883	38.959	1.00	16.91
5598	N	THR	A	834	34.820	-9.464	35.089	1.00	17.86
5599	CA	THR	A	834	34.456	-9.796	33.723	1.00	19.46
5600	C	THR	A	834	33.566	-8.753	33.065	1.00	18.40
5601	O	THR	A	834	32.831	-8.051	33.768	1.00	18.40
5602	CB	THR	A	834	33.710	-11.144	33.592	1.00	19.44
5603	OG1	THR	A	834	32.393	-10.968	34.125	1.00	20.68
5604	CG2	THR	A	834	34.421	-12.276	34.309	1.00	19.43
5605	N	ALA	A	835	33.566	-8.699	31.732	1.00	19.48
5606	CA	ALA	A	835	32.648	-7.803	31.033	1.00	20.00
5607	C	ALA	A	835	31.193	-8.165	31.312	1.00	20.77
5608	O	ALA	A	835	30.385	-7.248	31.410	1.00	22.50
5609	CB	ALA	A	835	32.842	-7.825	29.508	1.00	18.74
5610	N	ASP	A	836	30.790	-9.421	31.421	1.00	22.07
5611	CA	ASP	A	836	29.447	-9.864	31.696	1.00	23.30
5612	C	ASP	A	836	28.969	-9.388	33.066	1.00	21.99
5613	O	ASP	A	836	27.808	-9.041	33.223	1.00	22.47
5614	CB	ASP	A	836	29.282	-11.410	31.664	1.00	25.61
5615	CG	ASP	A	836	29.189	-11.927	30.230	1.00	27.82
5616	OD1	ASP	A	836	29.351	-13.150	30.024	1.00	30.02
5617	OD2	ASP	A	836	29.058	-11.147	29.276	1.00	26.35
5618	N	GLN	A	837	29.844	-9.310	34.063	1.00	21.84
5619	CA	GLN	A	837	29.453	-8.854	35.377	1.00	20.02
5620	C	GLN	A	837	29.051	-7.386	35.296	1.00	18.66
5621	O	GLN	A	837	28.053	-7.047	35.906	1.00	17.00
5622	CB	GLN	A	837	30.603	-8.904	36.400	1.00	21.90
5623	CG	GLN	A	837	30.712	-10.131	37.263	1.00	22.49
5624	CD	GLN	A	837	31.790	-9.982	38.343	1.00	21.99
5625	OE1	GLN	A	837	32.918	-9.616	38.024	1.00	20.17
5626	NE2	GLN	A	837	31.367	-10.297	39.564	1.00	20.64
5627	N	ILE	A	838	29.898	-6.608	34.623	1.00	16.54
5628	CA	ILE	A	838	29.667	-5.167	34.499	1.00	18.19
5629	C	ILE	A	838	28.370	-4.877	33.740	1.00	20.92
5630	O	ILE	A	838	27.578	-3.998	34.152	1.00	18.47
5631	CB	ILE	A	838	30.895	-4.516	33.835	1.00	19.11
5632	CG1	ILE	A	838	32.141	-4.578	34.778	1.00	16.48
5633	CG2	ILE	A	838	30.618	-3.062	33.428	1.00	18.17
5634	CD1	ILE	A	838	33.422	-4.259	33.992	1.00	16.81
5635	N	LYS	A	839	28.126	-5.604	32.642	1.00	20.40
5636	CA	LYS	A	839	26.868	-5.425	31.895	1.00	24.05
5637	C	LYS	A	839	25.681	-5.781	32.770	1.00	25.13
5638	O	LYS	A	839	24.646	-5.116	32.756	1.00	26.96
5639	CB	LYS	A	839	26.836	-6.328	30.636	1.00	24.14
5640	CG	LYS	A	839	27.894	-5.833	29.641	1.00	26.39
5641	CD	LYS	A	839	27.580	-6.351	28.235	1.00	30.49
5642	CE	LYS	A	839	28.219	-7.705	28.025	1.00	32.93
5643	NZ	LYS	A	839	28.865	-7.658	26.661	1.00	35.80
5644	N	GLN	A	840	25.788	-6.819	33.588	1.00	25.00
5645	CA	GLN	A	840	24.684	-7.184	34.471	1.00	26.52
5646	C	GLN	A	840	24.438	-6.235	35.642	1.00	24.27
5647	O	GLN	A	840	23.285	-6.041	36.067	1.00	21.92
5648	CB	GLN	A	840	25.070	-8.548	35.028	1.00	31.74
5649	CG	GLN	A	840	23.972	-9.403	35.610	1.00	39.43
5650	CD	GLN	A	840	24.253	-10.889	35.404	1.00	43.34
5651	OE1	GLN	A	840	23.875	-11.733	36.232	1.00	45.14
5652	NE2	GLN	A	840	24.920	-11.257	34.306	1.00	44.87
5653	N	ASN	A	841	25.494	-5.678	36.234	1.00	17.87
5654	CA	ASN	A	841	25.352	-4.940	37.483	1.00	19.33
5655	C	ASN	A	841	25.456	-3.442	37.474	1.00	17.58
5656	O	ASN	A	841	25.171	-2.831	38.520	1.00	17.51
5657	CB	ASN	A	841	26.468	-5.479	38.436	1.00	20.01
5658	CG	ASN	A	841	26.318	-6.928	38.823	1.00	21.30
5659	OD1	ASN	A	841	27.336	-7.581	39.153	1.00	24.17
5660	ND2	ASN	A	841	25.136	-7.506	38.867	1.00	17.31
5661	N	LEU	A	842	25.969	-2.825	36.425	1.00	17.66

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5662	CA	LEU	A	842	26.184	-1.376	36.377	1.00	17.63
5663	C	LEU	A	842	25.163	-0.724	35.461	1.00	18.99
5664	O	LEU	A	842	25.011	-1.186	34.306	1.00	17.85
5665	CB	LEU	A	842	27.657	-1.086	35.967	1.00	16.31
5666	CG	LEU	A	842	28.122	0.412	36.099	1.00	16.16
5667	CD1	LEU	A	842	29.646	0.464	36.201	1.00	15.40
5668	CD2	LEU	A	842	27.670	1.171	34.847	1.00	16.66
5669	N	THR	A	843	24.433	0.335	35.896	1.00	18.55
5670	CA	THR	A	843	23.509	0.996	34.955	1.00	19.55
5671	C	THR	A	843	23.799	2.485	35.083	1.00	18.14
5672	O	THR	A	843	23.954	2.940	36.217	1.00	18.37
5673	CB	THR	A	843	21.997	0.715	35.324	1.00	21.75
5674	OG1	THR	A	843	21.984	0.728	36.780	1.00	27.30
5675	CG2	THR	A	843	21.591	-0.733	35.145	1.00	20.25
5676	N	PHE	A	844	23.800	3.289	34.050	1.00	17.73
5677	CA	PHE	A	844	23.831	4.740	34.087	1.00	17.70
5678	C	PHE	A	844	22.432	5.276	34.395	1.00	19.50
5679	O	PHE	A	844	21.404	4.713	33.999	1.00	17.81
5680	CB	PHE	A	844	24.393	5.290	32.769	1.00	19.16
5681	CG	PHE	A	844	25.890	4.994	32.659	1.00	18.93
5682	CD1	PHE	A	844	26.336	3.998	31.778	1.00	19.58
5683	CD2	PHE	A	844	26.805	5.688	33.423	1.00	16.70
5684	CE1	PHE	A	844	27.691	3.718	31.666	1.00	17.53
5685	CE2	PHE	A	844	28.161	5.407	33.322	1.00	16.61
5686	CZ	PHE	A	844	28.604	4.408	32.474	1.00	16.03
5687	N	LEU	A	845	22.317	6.283	35.262	1.00	20.29
5688	CA	LEU	A	845	21.038	6.840	35.660	1.00	21.27
5689	C	LEU	A	845	20.919	8.200	34.954	1.00	23.53
5690	O	LEU	A	845	21.935	8.833	34.636	1.00	23.88
5691	CB	LEU	A	845	20.935	7.051	37.170	1.00	21.66
5692	CG	LEU	A	845	21.162	5.826	38.092	1.00	23.12
5693	CD1	LEU	A	845	21.274	6.272	39.546	1.00	22.17
5694	CD2	LEU	A	845	20.052	4.791	37.920	1.00	23.11
5695	N	GLU	A	846	19.690	8.626	34.698	1.00	21.38
5696	CA	GLU	A	846	19.490	9.929	34.070	1.00	24.30
5697	C	GLU	A	846	19.991	11.035	34.975	1.00	21.71
5698	O	GLU	A	846	19.653	11.010	36.172	1.00	20.11
5699	CB	GLU	A	846	17.975	10.166	33.842	1.00	28.61
5700	CG	GLU	A	846	17.724	11.373	32.965	1.00	34.76
5701	CD	GLU	A	846	17.726	12.749	33.588	1.00	39.53
5702	OE1	GLU	A	846	18.229	13.687	32.884	1.00	41.56
5703	OE2	GLU	A	846	17.272	13.005	34.732	1.00	40.66
5704	N	SER	A	847	20.680	12.026	34.430	1.00	19.82
5705	CA	SER	A	847	21.208	13.081	35.319	1.00	18.64
5706	C	SER	A	847	21.368	14.319	34.462	1.00	19.77
5707	O	SER	A	847	21.263	14.210	33.233	1.00	18.46
5708	CB	SER	A	847	22.527	12.667	36.002	1.00	17.95
5709	OG	SER	A	847	23.592	12.595	35.047	1.00	19.81
5710	N	PRO	A	848	21.622	15.466	35.068	1.00	20.84
5711	CA	PRO	A	848	21.738	16.711	34.326	1.00	21.84
5712	C	PRO	A	848	22.900	16.792	33.349	1.00	24.33
5713	O	PRO	A	848	23.896	16.064	33.439	1.00	22.58
5714	CB	PRO	A	848	21.911	17.756	35.428	1.00	21.32
5715	CG	PRO	A	848	21.153	17.200	36.614	1.00	21.13
5716	CD	PRO	A	848	21.503	15.705	36.538	1.00	20.99
5717	N	THR	A	849	22.785	17.738	32.406	1.00	24.17
5718	CA	THR	A	849	23.849	17.972	31.424	1.00	24.95
5719	C	THR	A	849	25.242	18.088	32.050	1.00	22.16
5720	O	THR	A	849	25.493	18.737	33.071	1.00	21.14
5721	CB	THR	A	849	23.540	19.287	30.661	1.00	24.81
5722	OG1	THR	A	849	22.271	19.114	30.029	1.00	25.94
5723	CG2	THR	A	849	24.626	19.557	29.609	1.00	25.93
5724	N	ASN	A	850	26.201	17.420	31.423	1.00	20.59
5725	CA	ASN	A	850	27.600	17.432	31.834	1.00	20.77
5726	C	ASN	A	850	27.795	16.847	33.239	1.00	19.84
5727	O	ASN	A	850	28.665	17.266	34.020	1.00	18.02
5728	CB	ASN	A	850	28.286	18.778	31.664	1.00	20.31
5729	CG	ASN	A	850	29.817	18.702	31.663	1.00	21.52
5730	OD1	ASN	A	850	30.384	17.768	31.100	1.00	19.79
5731	ND2	ASN	A	850	30.504	19.668	32.261	1.00	18.52
5732	N	THR	A	851	27.040	15.769	33.508	1.00	18.54
5733	CA	THR	A	851	27.234	14.985	34.728	1.00	19.54
5734	C	THR	A	851	27.138	13.496	34.402	1.00	19.84
5735	O	THR	A	851	26.541	13.150	33.375	1.00	18.01
5736	CB	THR	A	851	26.235	15.237	35.873	1.00	18.24
5737	OG1	THR	A	851	24.907	14.853	35.442	1.00	20.28
5738	CG2	THR	A	851	26.248	16.692	36.320	1.00	18.83
5739	N	VAL	A	852	27.723	12.627	35.230	1.00	18.35
5740	CA	VAL	A	852	27.673	11.190	34.978	1.00	18.50
5741	C	VAL	A	852	27.277	10.516	36.296	1.00	19.16
5742	O	VAL	A	852	28.012	10.724	37.265	1.00	16.89
5743	CB	VAL	A	852	29.064	10.638	34.571	1.00	20.21
5744	CG1	VAL	A	852	29.058	9.112	34.604	1.00	18.62
5745	CG2	VAL	A	852	29.530	11.124	33.192	1.00	17.86
5746	N	ALA	A	853	26.272	9.662	36.315	1.00	17.66
5747	CA	ALA	A	853	25.839	8.989	37.544	1.00	16.64
5748	C	ALA	A	853	25.511	7.540	37.210	1.00	17.67
5749	O	ALA	A	853	24.951	7.276	36.117	1.00	18.63
5750	CB	ALA	A	853	24.565	9.709	38.039	1.00	15.15
5751	N	PHE	A	854	25.863	6.606	38.068	1.00	16.51
5752	CA	PHE	A	854	25.701	5.180	37.832	1.00	17.75
5753	C	PHE	A	854	25.400	4.431	39.126	1.00	18.33
5754	O	PHE	A	854	25.573	4.950	40.251	1.00	19.36
5755	CB	PHE	A	854	26.922	4.577	37.103	1.00	18.03
5756	CG	PHE	A	854	28.266	4.665	37.791	1.00	18.64
5757	CD1	PHE	A	854	28.705	3.655	38.635	1.00	19.06

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5758	CD2	PHE	A	854	29.117	5.734	37.569	1.00	18.31
5759	CE1	PHE	A	854	29.952	3.745	39.251	1.00	17.32
5760	CE2	PHE	A	854	30.366	5.799	38.148	1.00	17.33
5761	CZ	PHE	A	854	30.793	4.792	39.003	1.00	15.66
5762	N	GLU	A	855	24.837	3.226	38.985	1.00	18.41
5763	CA	GLU	A	855	24.385	2.432	40.134	1.00	18.15
5764	C	GLU	A	855	24.952	1.008	40.033	1.00	17.60
5765	O	GLU	A	855	25.011	0.485	38.900	1.00	15.72
5766	CB	GLU	A	855	22.839	2.373	40.213	1.00	17.57
5767	CG	GLU	A	855	22.296	1.628	41.437	1.00	18.25
5768	CD	GLU	A	855	20.756	1.617	41.583	1.00	21.29
5769	OE1	GLU	A	855	20.194	1.168	42.603	1.00	18.85
5770	OE2	GLU	A	855	20.095	2.079	40.611	1.00	22.94
5771	N	LEU	A	856	25.606	0.580	41.096	1.00	17.21
5772	CA	LEU	A	856	26.188	-0.794	41.188	1.00	18.95
5773	C	LEU	A	856	25.172	-1.634	41.962	1.00	18.66
5774	O	LEU	A	856	24.868	-1.303	43.156	1.00	20.65
5775	CB	LEU	A	856	27.582	-0.729	41.838	1.00	15.58
5776	CG	LEU	A	856	28.600	0.261	41.242	1.00	15.91
5777	CD1	LEU	A	856	29.935	0.194	42.026	1.00	15.73
5778	CD2	LEU	A	856	28.851	-0.034	39.762	1.00	15.55
5779	N	LYS	A	857	24.482	-2.559	41.308	1.00	20.01
5780	CA	LYS	A	857	23.349	-3.244	41.916	1.00	21.47
5781	C	LYS	A	857	23.415	-4.614	42.559	1.00	19.85
5782	O	LYS	A	857	24.129	-5.512	42.141	1.00	16.38
5783	CB	LYS	A	857	22.273	-3.433	40.784	1.00	23.29
5784	CG	LYS	A	857	21.724	-2.106	40.284	1.00	26.57
5785	CD	LYS	A	857	20.895	-2.342	38.990	1.00	28.26
5786	CE	LYS	A	857	21.874	-2.829	37.915	1.00	29.07
5787	NZ	LYS	A	857	21.301	-3.488	36.718	1.00	28.50
5788	N	ASN	A	858	22.551	-4.779	43.556	1.00	20.08
5789	CA	ASN	A	858	22.342	-6.017	44.296	1.00	22.03
5790	C	ASN	A	858	23.574	-6.787	44.771	1.00	19.15
5791	O	ASN	A	858	23.832	-7.961	44.451	1.00	17.47
5792	CB	ASN	A	858	21.481	-6.963	43.428	1.00	24.99
5793	CG	ASN	A	858	20.672	-7.932	44.294	1.00	27.08
5794	OD1	ASN	A	858	20.308	-7.642	45.418	1.00	25.89
5795	ND2	ASN	A	858	20.346	-9.104	43.726	1.00	28.26
5796	N	TYR	A	859	24.290	-6.198	45.719	1.00	15.00
5797	CA	TYR	A	859	25.524	-6.732	46.272	1.00	15.84
5798	C	TYR	A	859	26.470	-7.231	45.162	1.00	14.81
5799	O	TYR	A	859	26.871	-8.386	45.149	1.00	13.23
5800	CB	TYR	A	859	25.147	-7.865	47.215	1.00	17.53
5801	CG	TYR	A	859	24.243	-7.457	48.362	1.00	18.89
5802	CD1	TYR	A	859	22.870	-7.641	48.244	1.00	20.51
5803	CD2	TYR	A	859	24.719	-6.915	49.548	1.00	17.97
5804	CE1	TYR	A	859	21.995	-7.319	49.262	1.00	20.07
5805	CE2	TYR	A	859	23.860	-6.602	50.574	1.00	18.09
5806	CZ	TYR	A	859	22.496	-6.786	50.428	1.00	21.56
5807	OH	TYR	A	859	21.657	-6.473	51.472	1.00	20.57
5808	N	ALA	A	860	26.756	-6.405	44.195	1.00	14.63
5809	CA	ALA	A	860	27.573	-6.753	43.030	1.00	16.97
5810	C	ALA	A	860	28.955	-7.249	43.442	1.00	18.77
5811	O	ALA	A	860	29.597	-6.651	44.336	1.00	19.26
5812	CB	ALA	A	860	27.744	-5.511	42.164	1.00	18.48
5813	N	ASN	A	861	29.362	-8.365	42.860	1.00	18.35
5814	CA	ASN	A	861	30.655	-8.995	43.164	1.00	18.84
5815	C	ASN	A	861	30.855	-9.139	44.672	1.00	19.08
5816	O	ASN	A	861	31.935	-8.866	45.226	1.00	18.01
5817	CB	ASN	A	861	31.796	-8.205	42.485	1.00	18.52
5818	CG	ASN	A	861	33.144	-8.920	42.430	1.00	18.65
5819	OD1	ASN	A	861	33.182	-10.129	42.202	1.00	18.09
5820	ND2	ASN	A	861	34.255	-8.206	42.638	1.00	16.42
5821	N	HIS	A	862	29.923	-9.745	45.420	1.00	18.36
5822	CA	HIS	A	862	29.912	-10.026	46.835	1.00	18.01
5823	C	HIS	A	862	30.326	-8.786	47.655	1.00	18.23
5824	O	HIS	A	862	31.071	-8.845	48.634	1.00	19.60
5825	CB	HIS	A	862	30.725	-11.267	47.307	1.00	18.46
5826	CG	HIS	A	862	32.194	-11.226	46.999	1.00	20.04
5827	ND1	HIS	A	862	32.690	-11.802	45.836	1.00	21.25
5828	CD2	HIS	A	862	33.279	-10.659	47.560	1.00	21.51
5829	CE1	HIS	A	862	33.983	-11.616	45.725	1.00	21.85
5830	NE2	HIS	A	862	34.380	-10.896	46.767	1.00	23.07
5831	N	ASP	A	863	29.770	-7.637	47.354	1.00	16.12
5832	CA	ASP	A	863	29.883	-6.424	48.130	1.00	17.57
5833	C	ASP	A	863	28.980	-6.498	49.361	1.00	16.17
5834	O	ASP	A	863	27.999	-7.241	49.361	1.00	15.89
5835	CB	ASP	A	863	29.435	-5.250	47.242	1.00	17.41
5836	CG	ASP	A	863	30.045	-3.935	47.687	1.00	19.24
5837	OD1	ASP	A	863	31.158	-3.597	47.207	1.00	15.53
5838	OD2	ASP	A	863	29.459	-3.191	48.509	1.00	20.34
5839	N	THR	A	864	29.270	-5.700	50.388	1.00	16.93
5840	CA	THR	A	864	28.442	-5.615	51.570	1.00	17.66
5841	C	THR	A	864	27.315	-4.585	51.445	1.00	19.37
5842	O	THR	A	864	26.382	-4.558	52.256	1.00	19.59
5843	CB	THR	A	864	29.230	-5.242	52.846	1.00	18.03
5844	OG1	THR	A	864	30.031	-4.081	52.545	1.00	18.52
5845	CG2	THR	A	864	30.062	-6.428	53.337	1.00	17.90
5846	N	TRP	A	865	27.378	-3.754	50.419	1.00	18.22
5847	CA	TRP	A	865	26.366	-2.703	50.191	1.00	19.88
5848	C	TRP	A	865	25.478	-3.241	49.072	1.00	21.10
5849	O	TRP	A	865	25.965	-3.703	48.039	1.00	19.83
5850	CB	TRP	A	865	27.055	-1.385	49.870	1.00	20.11
5851	CG	TRP	A	865	27.697	-0.603	50.975	1.00	20.00
5852	CD1	TRP	A	865	27.512	-0.899	52.310	1.00	20.46
5853	CD2	TRP	A	865	28.490	0.608	50.952	1.00	19.16

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5854	NE1	TRP	A	865	28.207	-0.016	53.072	1.00	19.59
5855	CE2	TRP	A	865	28.808	0.918	52.281	1.00	20.04
5856	CE3	TRP	A	865	29.016	1.392	49.936	1.00	18.40
5857	CZ2	TRP	A	865	29.584	2.019	52.639	1.00	19.58
5858	CZ3	TRP	A	865	29.777	2.502	50.287	1.00	20.06
5859	CH2	TRP	A	865	30.082	2.782	51.624	1.00	18.82
5860	N	LYS	A	866	24.171	-3.257	49.278	1.00	18.45
5861	CA	LYS	A	866	23.184	-3.732	48.319	1.00	20.04
5862	C	LYS	A	866	23.133	-2.967	47.004	1.00	19.12
5863	O	LYS	A	866	23.316	-3.533	45.926	1.00	16.36
5864	CB	LYS	A	866	21.813	-3.689	49.002	1.00	20.69
5865	CG	LYS	A	866	20.635	-4.165	48.181	1.00	25.35
5866	CD	LYS	A	866	19.462	-4.533	49.094	1.00	30.56
5867	CE	LYS	A	866	18.162	-4.133	48.385	1.00	32.55
5868	NZ	LYS	A	866	17.703	-5.263	47.516	1.00	36.93
5869	N	ASN	A	867	22.957	-1.640	47.085	1.00	17.81
5870	CA	ASN	A	867	22.992	-0.817	45.878	1.00	19.57
5871	C	ASN	A	867	23.954	0.339	46.119	1.00	19.05
5872	O	ASN	A	867	23.947	0.830	47.255	1.00	17.99
5873	CB	ASN	A	867	21.656	-0.244	45.428	1.00	19.15
5874	CG	ASN	A	867	20.650	-1.322	45.045	1.00	20.68
5875	OD1	ASN	A	867	20.987	-2.249	44.295	1.00	20.32
5876	ND2	ASN	A	867	19.422	-1.255	45.549	1.00	17.97
5877	N	ILE	A	868	24.751	0.805	45.213	1.00	18.06
5878	CA	ILE	A	868	25.644	1.902	45.360	1.00	17.77
5879	C	ILE	A	868	25.425	2.872	44.217	1.00	17.69
5880	O	ILE	A	868	25.330	2.391	43.094	1.00	18.10
5881	CB	ILE	A	868	27.127	1.424	45.318	1.00	18.75
5882	CG1	ILE	A	868	27.433	0.426	46.467	1.00	19.10
5883	CG2	ILE	A	868	28.041	2.639	45.602	1.00	18.17
5884	CD1	ILE	A	868	28.866	-0.183	46.382	1.00	19.08
5885	N	ILE	A	869	25.397	4.154	44.510	1.00	16.22
5886	CA	ILE	A	869	25.256	5.150	43.447	1.00	15.16
5887	C	ILE	A	869	26.496	6.039	43.528	1.00	15.96
5888	O	ILE	A	869	26.936	6.380	44.637	1.00	17.68
5889	CB	ILE	A	869	23.932	5.949	43.590	1.00	14.79
5890	CG1	ILE	A	869	22.753	5.177	43.024	1.00	16.18
5891	CG2	ILE	A	869	24.060	7.342	42.951	1.00	14.77
5892	CD1	ILE	A	869	21.309	5.688	43.251	1.00	17.74
5893	N	VAL	A	870	27.084	6.345	42.385	1.00	13.11
5894	CA	VAL	A	870	28.208	7.276	42.308	1.00	15.88
5895	C	VAL	A	870	27.777	8.403	41.357	1.00	13.78
5896	O	VAL	A	870	27.303	8.071	40.277	1.00	14.36
5897	CB	VAL	A	870	29.500	6.597	41.787	1.00	16.19
5898	CG1	VAL	A	870	30.634	7.584	41.464	1.00	17.02
5899	CG2	VAL	A	870	29.989	5.575	42.845	1.00	15.31
5900	N	MET	A	871	28.093	9.657	41.556	1.00	15.32
5901	CA	MET	A	871	27.849	10.659	40.508	1.00	16.32
5902	C	MET	A	871	28.985	11.671	40.520	1.00	16.77
5903	O	MET	A	871	29.341	12.115	41.624	1.00	16.61
5904	CB	MET	A	871	26.511	11.402	40.645	1.00	17.18
5905	CG	MET	A	871	26.303	12.711	39.875	1.00	18.06
5906	SD	MET	A	871	24.576	13.307	40.042	1.00	17.89
5907	CE	MET	A	871	24.717	14.958	39.345	1.00	17.65
5908	N	TYR	A	872	29.496	11.964	39.333	1.00	15.67
5909	CA	TYR	A	872	30.520	13.001	39.181	1.00	17.64
5910	C	TYR	A	872	29.866	14.313	38.765	1.00	17.57
5911	O	TYR	A	872	29.125	14.271	37.786	1.00	18.01
5912	CB	TYR	A	872	31.569	12.699	38.081	1.00	16.70
5913	CG	TYR	A	872	32.156	11.318	38.208	1.00	16.28
5914	CD1	TYR	A	872	32.120	10.472	37.110	1.00	13.82
5915	CD2	TYR	A	872	32.651	10.833	39.432	1.00	17.04
5916	CE1	TYR	A	872	32.631	9.180	37.193	1.00	15.56
5917	CE2	TYR	A	872	33.138	9.522	39.527	1.00	16.23
5918	CZ	TYR	A	872	33.069	8.696	38.405	1.00	16.02
5919	OH	TYR	A	872	33.528	7.402	38.433	1.00	16.10
5920	N	ASN	A	873	30.114	15.425	39.416	1.00	18.25
5921	CA	ASN	A	873	29.599	16.720	39.021	1.00	17.41
5922	C	ASN	A	873	30.804	17.644	38.874	1.00	17.53
5923	O	ASN	A	873	31.181	18.240	39.867	1.00	18.67
5924	CB	ASN	A	873	28.650	17.362	40.055	1.00	18.79
5925	CG	ASN	A	873	28.169	18.759	39.681	1.00	19.71
5926	OD1	ASN	A	873	28.219	19.179	38.513	1.00	19.99
5927	ND2	ASN	A	873	27.768	19.612	40.630	1.00	16.40
5928	N	PRO	A	874	31.324	17.850	37.673	1.00	17.92
5929	CA	PRO	A	874	32.426	18.758	37.448	1.00	18.85
5930	C	PRO	A	874	31.964	20.201	37.260	1.00	20.43
5931	O	PRO	A	874	32.857	21.062	37.114	1.00	19.83
5932	CB	PRO	A	874	33.028	18.250	36.120	1.00	18.54
5933	CG	PRO	A	874	31.814	17.776	35.350	1.00	18.34
5934	CD	PRO	A	874	30.927	17.154	36.432	1.00	18.38
5935	N	ASN	A	875	30.658	20.487	37.266	1.00	18.81
5936	CA	ASN	A	875	30.197	21.862	37.056	1.00	21.71
5937	C	ASN	A	875	30.401	22.836	38.198	1.00	21.33
5938	O	ASN	A	875	30.422	22.397	39.369	1.00	20.55
5939	CB	ASN	A	875	28.687	21.786	36.701	1.00	22.52
5940	CG	ASN	A	875	28.451	20.853	35.519	1.00	24.12
5941	OD1	ASN	A	875	28.894	21.182	34.417	1.00	26.00
5942	ND2	ASN	A	875	27.799	19.711	35.664	1.00	21.36
5943	N	LYS	A	876	30.486	24.146	37.974	1.00	21.86
5944	CA	LYS	A	876	30.645	25.159	39.028	1.00	25.54
5945	C	LYS	A	876	29.380	25.447	39.861	1.00	23.68
5946	O	LYS	A	876	29.408	26.291	40.768	1.00	20.96
5947	CB	LYS	A	876	31.049	26.536	38.435	1.00	28.74
5948	CG	LYS	A	876	32.446	26.518	37.768	1.00	32.96
5949	CD	LYS	A	876	33.382	26.138	38.926	1.00	35.88

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5950	CE	LYS	A	876	34.570	27.098	39.033	1.00	37.37
5951	NZ	LYS	A	876	35.469	26.778	37.875	1.00	36.83
5952	N	THR	A	877	28.261	24.779	39.591	1.00	22.70
5953	CA	THR	A	877	27.057	24.946	40.425	1.00	22.49
5954	C	THR	A	877	26.579	23.547	40.821	1.00	21.81
5955	O	THR	A	877	26.865	22.555	40.163	1.00	19.74
5956	CB	THR	A	877	25.891	25.589	39.673	1.00	22.36
5957	OG1	THR	A	877	25.632	24.830	38.499	1.00	23.54
5958	CG2	THR	A	877	26.212	27.030	39.271	1.00	25.23
5959	N	SER	A	878	25.857	23.541	41.955	1.00	18.08
5960	CA	SER	A	878	25.326	22.269	42.406	1.00	18.86
5961	C	SER	A	878	24.284	21.737	41.420	1.00	19.86
5962	O	SER	A	878	23.661	22.481	40.673	1.00	18.20
5963	CB	SER	A	878	24.366	22.598	43.617	1.00	16.87
5964	OG	SER	A	878	23.469	23.709	43.603	1.00	20.00
5965	N	GLN	A	879	24.144	20.400	41.475	1.00	20.32
5966	CA	GLN	A	879	23.180	19.790	40.580	1.00	21.86
5967	C	GLN	A	879	22.200	18.733	41.224	1.00	22.97
5968	O	GLN	A	879	22.675	18.029	42.131	1.00	21.65
5969	CB	GLN	A	879	23.931	18.974	39.468	1.00	22.37
5970	CG	GLN	A	879	24.910	19.802	38.645	1.00	22.60
5971	CD	GLN	A	879	24.240	20.815	37.750	1.00	23.49
5972	OE1	GLN	A	879	23.305	20.445	37.029	1.00	24,49
5973	NE2	GLN	A	879	24.740	22.035	37.686	1.00	23.81
5974	N	THR	A	880	20.980	18.539	40.721	1.00	20.70
5975	CA	THR	A	880	20.040	17.652	41.394	1.00	21.62
5976	C	THR	A	880	19.919	16.302	40.713	1.00	18.77
5977	O	THR	A	880	19.923	16.258	39.513	1.00	18.27
5978	CB	THR	A	880	18.613	18.275	41.489	1.00	25.07
5979	OG1	THR	A	880	18.717	19.445	42.338	1.00	27.52
5980	CG2	THR	A	880	17.672	17.294	42.200	1.00	26.46
5981	N	LEU	A	881	20.041	15.196	41.424	1.00	17.50
5982	CA	LEU	A	881	19.883	13.866	40.872	1.00	17.31
5983	C	LEU	A	881	18.575	13.262	41.401	1.00	17.89
5984	O	LEU	A	881	18.363	13.335	42.617	1.00	17.14
5985	CB	LEU	A	881	21.058	12.982	41.365	1.00	18.29
5986	CG	LEU	A	881	21.001	11.492	41.039	1.00	20.54
5987	CD1	LEU	A	881	21.214	11.306	39.528	1.00	21.58
5988	CD2	LEU	A	881	22.087	10.699	41.817	1.00	20.54
5989	N	ASN	A	882	17.745	12.668	40.578	1.00	18.74
5990	CA	ASN	A	882	16.529	11.983	40.974	1.00	20.32
5991	C	ASN	A	882	16.916	10.547	41.262	1.00	19.51
5992	O	ASN	A	882	17.686	9.944	40.505	1.00	21.26
5993	CB	ASN	A	882	15.547	12.040	39.832	1.00	24.52
5994	CG	ASN	A	882	15.024	13.451	39.705	1.00	27.48
5995	OD1	ASN	A	882	14.600	14.087	40.666	1.00	28.76
5996	ND2	ASN	A	882	15.063	13.946	38.456	1.00	20.00
5997	N	LEU	A	883	16.404	9.998	42.341	1.00	20.69
5998	CA	LEU	A	883	16.795	8.686	42.799	1.00	19.88
5999	C	LEU	A	883	15.783	7.565	42.619	1.00	21.80
6000	O	LEU	A	883	14.583	7.773	42.723	1.00	23.04
6001	CB	LEU	A	883	17.076	8.771	44.330	1.00	19.20
6002	CG	LEU	A	883	18.161	9.773	44.743	1.00	19.84
6003	CD1	LEU	A	883	18.166	10.045	46.259	1.00	20.56
6004	CD2	LEU	A	883	19.510	9.241	44.291	1.00	15.99
6005	N	PRO	A	884	16.303	6.364	42.482	1.00	20.55
6006	CA	PRO	A	884	15.498	5.168	42.474	1.00	23.11
6007	C	PRO	A	884	14.757	5.106	43.809	1.00	22.93
6008	O	PRO	A	884	15.119	5.780	44.796	1.00	21.23
6009	CB	PRO	A	884	16.530	4.053	42.301	1.00	22.91
6010	CG	PRO	A	884	17.714	4.713	41.660	1.00	21.54
6011	CD	PRO	A	884	17.762	6.046	42.397	1.00	20.96
6012	N	SER	A	885	13.760	4.240	43.934	1.00	21.66
6013	CA	SER	A	885	12.967	4.273	45.162	1.00	24.40
6014	C	SER	A	885	13.716	3.881	46.431	1.00	23.95
6015	O	SER	A	885	14.814	3.285	46.467	1.00	21.34
6016	CB	SER	A	885	11.706	3.395	44.996	1.00	25.34
6017	OG	SER	A	885	12.206	2.088	45.063	1.00	26.34
6018	N	GLY	A	886	13.117	4.365	47.544	1.00	21.95
6019	CA	GLY	A	886	13.647	3.960	48.850	1.00	21.89
6020	C	GLY	A	886	14.483	4.998	49.573	1.00	22.67
6021	O	GLY	A	886	14.689	6.146	49.165	1.00	23.42
6022	N	ASP	A	887	14.869	4.680	50.801	1.00	21.05
6023	CA	ASP	A	887	15.760	5.451	51.645	1.00	22.50
6024	C	ASP	A	887	17.214	5.281	51.210	1.00	20.68
6025	O	ASP	A	887	17.634	4.130	51.040	1.00	19.39
6026	CB	ASP	A	887	15.602	4.969	53.086	1.00	23.02
6027	CG	ASP	A	887	16.484	5.799	54.001	1.00	25.67
6028	OD1	ASP	A	887	17.638	5.419	54.199	1.00	28.60
6029	OD2	ASP	A	887	16.009	6.815	54.502	1.00	20.00
6030	N	TRP	A	888	17.977	6.376	51.081	1.00	19.72
6031	CA	TRP	A	888	19.375	6.298	50.691	1.00	17.29
6032	C	TRP	A	888	20.292	6.887	51.745	1.00	18.92
6033	O	TRP	A	888	19.985	7.977	52.265	1.00	19.35
6034	CB	TRP	A	888	19.584	6.970	49.305	1.00	19.14
6035	CG	TRP	A	888	19.041	6.188	48.135	1.00	21.37
6036	CD1	TRP	A	888	17.777	6.307	47.614	1.00	19.94
6037	CD2	TRP	A	888	19.692	5.196	47.325	1.00	21.02
6038	NE1	TRP	A	888	17.616	5.449	46.549	1.00	20.33
6039	CE2	TRP	A	888	18.775	4.742	46.365	1.00	21.10
6040	CE3	TRP	A	888	20.966	4.626	47.345	1.00	23.66
6041	CZ2	TRP	A	888	19.060	3.727	45.435	1.00	20.78
6042	CZ3	TRP	A	888	21.271	3.645	46.396	1.00	23.95
6043	CH2	TRP	A	888	20.330	3.181	45.469	1.00	21.41
6044	N	THR	A	889	21.444	6.290	52.074	1.00	16.86
6045	CA	THR	A	889	22.397	6.862	53.008	1.00	17.70

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6046	C	THR A 889	23.506	7.623	52.293	1.00	18.48
6047	O	THR A 889	24.068	7.059	51.330	1.00	17.19
6048	CB	THR A 889	23.071	5.754	53.870	1.00	18.89
6049	OG1	THR A 889	22.031	5.014	54.495	1.00	19.06
6050	CG2	THR A 889	23.995	6.360	54.928	1.00	16.36
6051	N	ILE A 890	23.827	8.864	52.643	1.00	17.13
6052	CA	ILE A 890	24.908	9.575	51.956	1.00	18.82
6053	C	ILE A 890	26.259	9.160	52.591	1.00	18.09
6054	O	ILE A 890	26.349	9.198	53.816	1.00	18.88
6055	CB	ILE A 890	24.732	11.089	52.093	1.00	18.96
6056	CG1	ILE A 890	23.367	11.573	51.535	1.00	19.44
6057	CG2	ILE A 890	25.920	11.771	51.420	1.00	15.34
6058	CD1	ILE A 890	23.069	12.988	52.057	1.00	19.01
6059	N	VAL A 891	27.241	8.700	51.844	1.00	17.95
6060	CA	VAL A 891	28.536	8.307	52.362	1.00	17.49
6061	C	VAL A 891	29.719	9.089	51.748	1.00	17.57
6062	O	VAL A 891	30.808	9.192	52.354	1.00	16.92
6063	CB	VAL A 891	28.904	6.821	52.307	1.00	18.15
6064	CG1	VAL A 891	27.983	6.048	53.233	1.00	19.10
6065	CG2	VAL A 891	28.997	6.205	50.921	1.00	18.18
6066	N	GLY A 892	29.413	9.810	50.684	1.00	14.68
6067	CA	GLY A 892	30.419	10.659	50.046	1.00	15.77
6068	C	GLY A 892	29.792	12.007	49.641	1.00	18.34
6069	O	GLY A 892	28.876	11.911	48.821	1.00	15.50
6070	N	LEU A 893	30.225	13.102	50.237	1.00	17.98
6071	CA	LEU A 893	29.668	14.397	49.870	1.00	18.16
6072	C	LEU A 893	30.721	15.469	50.156	1.00	18.84
6073	O	LEU A 893	31.329	15.577	51.225	1.00	18.84
6074	CB	LEU A 893	28.353	14.725	50.598	1.00	18.93
6075	CG	LEU A 893	27.657	16.052	50.223	1.00	20.31
6076	CD1	LEU A 893	26.160	15.915	50.545	1.00	19.83
6077	CD2	LEU A 893	28.199	17.314	50.895	1.00	19.07
6078	N	GLY A 894	30.863	16.384	49.199	1.00	18.44
6079	CA	GLY A 894	31.780	17.536	49.376	1.00	19.33
6080	C	GLY A 894	33.173	16.936	49.592	1.00	21.53
6081	O	GLY A 894	33.534	16.015	48.857	1.00	20.54
6082	N	ASP A 895	33.906	17.393	50.605	1.00	20.89
6083	CA	ASP A 895	35.240	16.835	50.842	1.00	22.34
6084	C	ASP A 895	35.191	15.680	51.834	1.00	22.18
6085	O	ASP A 895	36.127	15.514	52.615	1.00	24.94
6086	CB	ASP A 895	36.130	17.947	51.393	1.00	22.12
6087	CG	ASP A 895	35.478	18.553	52.622	1.00	23.64
6088	OD1	ASP A 895	36.022	19.522	53.153	1.00	25.64
6089	OD2	ASP A 895	34.435	18.052	53.033	1.00	20.00
6090	N	GLN A 896	34.086	14.968	51.966	1.00	22.81
6091	CA	GLN A 896	33.930	13.925	52.976	1.00	22.65
6092	C	GLN A 896	33.662	12.612	52.237	1.00	22.28
6093	O	GLN A 896	32.744	12.496	51.436	1.00	19.57
6094	CB	GLN A 896	32.781	14.173	53.958	1.00	24.18
6095	CG	GLN A 896	32.835	15.288	54.933	1.00	28.13
6096	CD	GLN A 896	32.024	15.444	56.200	1.00	30.70
6097	OE1	GLN A 896	32.333	15.046	57.385	1.00	31.20
6098	NE2	GLN A 896	30.906	16.146	56.043	1.00	23.23
6099	N	ILE A 897	34.546	11.646	52.545	1.00	20.05
6100	CA	ILE A 897	34.366	10.348	51.925	1.00	19.25
6101	C	ILE A 897	34.674	9.206	53.003	1.00	17.61
6102	O	ILE A 897	35.565	9.391	53.822	1.00	17.24
6103	CB	ILE A 897	35.364	9.778	50.777	1.00	21.18
6104	CG1	ILE A 897	35.494	11.058	49.949	1.00	19.62
6105	CG2	ILE A 897	34.751	8.692	49.874	1.00	24.68
6106	CD1	ILE A 897	34.203	10.877	49.148	1.00	20.00
6107	N	GLY A 898	33.824	8.166	53.012	1.00	18.75
6108	CA	GLY A 898	34.047	7.122	53.993	1.00	19.72
6109	C	GLY A 898	32.917	6.112	54.045	1.00	21.21
6110	O	GLY A 898	32.131	6.024	53.098	1.00	22.52
6111	N	GLU A 899	32.839	5.374	55.134	1.00	22.66
6112	CA	GLU A 899	31.848	4.331	55.295	1.00	24.68
6113	C	GLU A 899	30.672	4.756	56.173	1.00	25.01
6114	O	GLU A 899	29.690	4.011	56.229	1.00	25.22
6115	CB	GLU A 899	32.539	3.087	55.883	1.00	25.95
6116	CG	GLU A 899	33.810	2.569	55.207	1.00	25.09
6117	CD	GLU A 899	33.525	1.712	53.981	1.00	25.77
6118	OE1	GLU A 899	32.401	1.155	53.967	1.00	25.14
6119	OE2	GLU A 899	34.413	1.517	53.062	1.00	24.44
6120	N	LYS A 900	30.700	5.917	56.818	1.00	26.68
6121	CA	LYS A 900	29.588	6.315	57.712	1.00	27.25
6122	C	LYS A 900	28.562	7.272	57.137	1.00	25.12
6123	O	LYS A 900	28.877	8.021	56.214	1.00	24.34
6124	CB	LYS A 900	30.138	6.954	58.991	1.00	30.47
6125	CG	LYS A 900	31.166	8.056	58.815	1.00	34.16
6126	CD	LYS A 900	31.252	8.901	60.073	1.00	37.55
6127	CE	LYS A 900	32.148	10.117	60.043	1.00	39.40
6128	NZ	LYS A 900	31.814	11.176	59.022	1.00	39.28
6129	N	SER A 901	27.347	7.305	57.686	1.00	22.18
6130	CA	SER A 901	26.272	8.150	57.221	1.00	19.86
6131	C	SER A 901	26.602	9.636	57.424	1.00	20.90
6132	O	SER A 901	26.916	10.105	58.520	1.00	17.48
6133	CB	SER A 901	24.943	7.837	57.959	1.00	20.68
6134	OG	SER A 901	23.889	8.727	57.561	1.00	20.53
6135	N	LEU A 902	26.313	10.398	56.397	1.00	20.11
6136	CA	LEU A 902	26.356	11.850	56.363	1.00	21.86
6137	C	LEU A 902	24.905	12.352	56.257	1.00	21.44
6138	O	LEU A 902	24.619	13.483	55.884	1.00	23.50
6139	CB	LEU A 902	27.161	12.292	55.123	1.00	20.45
6140	CG	LEU A 902	28.648	11.907	55.124	1.00	21.85
6141	CD1	LEU A 902	29.313	12.215	53.787	1.00	21.36

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6142	CD2	LEU	A	902	29.429	12.647	56.213	1.00	23.54
6143	N	GLY	A	903	23.941	11.490	56.527	1.00	22.23
6144	CA	GLY	A	903	22.507	11.805	56.400	1.00	21.35
6145	C	GLY	A	903	21.755	10.820	55.503	1.00	22.85
6146	O	GLY	A	903	22.304	9.974	54.773	1.00	21.12
6147	N	HIS	A	904	20.416	10.897	55.544	1.00	21.69
6148	CA	HIS	A	904	19.535	10.011	54.797	1.00	23.46
6149	C	HIS	A	904	18.628	10.789	53.870	1.00	23.10
6150	O	HIS	A	904	18.198	11.869	54.301	1.00	24.57
6151	CB	HIS	A	904	18.698	9.166	55.765	1.00	24.48
6152	CG	HIS	A	904	19.422	8.024	56.402	1.00	25.51
6153	ND1	HIS	A	904	20.109	8.146	57.599	1.00	26.84
6154	CD2	HIS	A	904	19.509	6.720	56.060	1.00	25.70
6155	CE1	HIS	A	904	20.654	6.968	57.906	1.00	24.89
6156	NE2	HIS	A	904	20.287	6.092	57.025	1.00	26.58
6157	N	VAL	A	905	18.379	10.385	52.631	1.00	20.66
6158	CA	VAL	A	905	17.530	11.105	51.710	1.00	21.55
6159	C	VAL	A	905	16.686	10.142	50.856	1.00	22.40
6160	O	VAL	A	905	16.926	8.935	50.724	1.00	21.14
6161	CB	VAL	A	905	18.271	12.035	50.716	1.00	22.34
6162	CG1	VAL	A	905	19.182	13.071	51.320	1.00	22.74
6163	CG2	VAL	A	905	19.108	11.151	49.778	1.00	22.37
6164	N	MET	A	906	15.637	10.699	50.260	1.00	21.77
6165	CA	MET	A	906	14.755	9.959	49.363	1.00	24.07
6166	C	MET	A	906	14.160	10.924	48.328	1.00	23.61
6167	O	MET	A	906	14.031	12.130	48.524	1.00	22.79
6168	CB	MET	A	906	13.578	9.416	50.195	1.00	26.81
6169	CG	MET	A	906	12.397	10.208	50.760	1.00	32.84
6170	SD	MET	A	906	11.387	9.012	51.643	1.00	20.00
6171	CE	MET	A	906	11.948	7.311	51.468	1.00	20.00
6172	N	GLY	A	907	13.907	10.353	47.148	1.00	21.83
6173	CA	GLY	A	907	13.278	11.077	46.048	1.00	21.53
6174	C	GLY	A	907	14.374	11.725	45.200	1.00	20.44
6175	O	GLY	A	907	14.554	11.417	44.029	1.00	18.16
6176	N	ASN	A	908	15.070	12.662	45.868	1.00	20.78
6177	CA	ASN	A	908	16.156	13.320	45.167	1.00	21.15
6178	C	ASN	A	908	17.211	13.868	46.130	1.00	20.98
6179	O	ASN	A	908	17.017	13.926	47.338	1.00	18.52
6180	CB	ASN	A	908	15.571	14.503	44.390	1.00	25.44
6181	CG	ASN	A	908	15.149	15.737	45.145	1.00	20.00
6182	OD1	ASN	A	908	14.950	16.900	44.807	1.00	20.00
6183	ND2	ASN	A	908	14.852	15.267	46.369	1.00	20.00
6184	N	VAL	A	909	18.336	14.263	45.507	1.00	18.91
6185	CA	VAL	A	909	19.404	14.800	46.327	1.00	18.32
6186	C	VAL	A	909	20.288	15.881	45.643	1.00	18.88
6187	O	VAL	A	909	20.470	15.801	44.414	1.00	16.18
6188	CB	VAL	A	909	20.296	13.598	46.765	1.00	17.97
6189	CG1	VAL	A	909	20.923	12.911	45.546	1.00	19.38
6190	CG2	VAL	A	909	21.470	13.978	47.699	1.00	17.98
6191	N	GLN	A	910	20.764	16.892	46.388	1.00	17.12
6192	CA	GLN	A	910	21.594	17.918	45.745	1.00	19.67
6193	C	GLN	A	910	23.093	17.606	45.891	1.00	20.86
6194	O	GLN	A	910	23.536	17.338	47.015	1.00	17.07
6195	CB	GLN	A	910	21.229	19.312	46.287	1.00	22.85
6196	CG	GLN	A	910	19.856	19.985	46.266	1.00	27.05
6197	CD	GLN	A	910	19.701	21.417	46.720	1.00	30.96
6198	OE1	GLN	A	910	20.065	22.155	45.819	1.00	34.28
6199	NE2	GLN	A	910	19.496	21.840	47.984	1.00	20.00
6200	N	VAL	A	911	23.796	17.686	44.736	1.00	19.28
6201	CA	VAL	A	911	25.245	17.405	44.720	1.00	17.62
6202	C	VAL	A	911	26.083	18.669	44.564	1.00	16.72
6203	O	VAL	A	911	25.929	19.417	43.604	1.00	15.75
6204	CB	VAL	A	911	25.554	16.486	43.522	1.00	18.06
6205	CG1	VAL	A	911	27.073	16.218	43.441	1.00	17.92
6206	CG2	VAL	A	911	24.732	15.197	43.636	1.00	17.78
6207	N	PRO	A	912	27.026	18.916	45.461	1.00	16.38
6208	CA	PRO	A	912	27.871	20.082	45.470	1.00	17.42
6209	C	PRO	A	912	28.675	20.351	44.198	1.00	18.48
6210	O	PRO	A	912	29.107	19.443	43.466	1.00	16.06
6211	CB	PRO	A	912	28.858	19.807	46.625	1.00	18.95
6212	CG	PRO	A	912	28.014	19.010	47.577	1.00	18.32
6213	CD	PRO	A	912	27.262	18.053	46.667	1.00	17.58
6214	N	ALA	A	913	28.947	21.637	43.934	1.00	18.47
6215	CA	ALA	A	913	29.792	21.934	42.767	1.00	18.97
6216	C	ALA	A	913	31.156	21.235	42.809	1.00	19.12
6217	O	ALA	A	913	31.887	21.154	43.805	1.00	18.44
6218	CB	ALA	A	913	30.037	23.434	42.685	1.00	19.77
6219	N	ILE	A	914	31.633	20.856	41.633	1.00	18.72
6220	CA	ILE	A	914	32.920	20.212	41.447	1.00	19.25
6221	C	ILE	A	914	33.188	19.086	42.437	1.00	17.77
6222	O	ILE	A	914	34.174	19.116	43.194	1.00	14.80
6223	CB	ILE	A	914	34.148	21.132	41.309	1.00	23.32
6224	CG1	ILE	A	914	34.131	22.434	40.505	1.00	20.00
6225	CG2	ILE	A	914	35.175	20.189	40.657	1.00	20.00
6226	CD1	ILE	A	914	35.357	23.346	40.425	1.00	27.60
6227	N	SER	A	915	32.382	18.019	42.461	1.00	16.85
6228	CA	SER	A	915	32.568	16.964	43.470	1.00	17.87
6229	C	SER	A	915	31.956	15.634	43.080	1.00	16.66
6230	O	SER	A	915	31.365	15.476	42.014	1.00	16.70
6231	CB	SER	A	915	31.875	17.394	44.797	1.00	19.13
6232	OG	SER	A	915	30.465	17.164	44.596	1.00	18.25
6233	N	THR	A	916	32.324	14.578	43.799	1.00	15.50
6234	CA	THR	A	916	31.790	13.243	43.594	1.00	13.88
6235	C	THR	A	916	30.813	12.945	44.738	1.00	16.32
6236	O	THR	A	916	31.111	13.139	45.938	1.00	16.25
6237	CB	THR	A	916	32.932	12.214	43.565	1.00	15.91

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6238	OG1	THR	A	916	33.805	12.538	42.444	1.00	16.29
6239	CG2	THR	A	916	32.413	10.796	43.465	1.00	15.30
6240	N	LEU	A	917	29.643	12.422	44.406	1.00	18.04
6241	CA	LEU	A	917	28.642	12.007	45.400	1.00	19.93
6242	C	LEU	A	917	28.612	10.487	45.449	1.00	18.73
6243	O	LEU	A	917	28.780	9.832	44.413	1.00	19.02
6244	CB	LEU	A	917	27.290	12.536	44.972	1.00	20.24
6245	CG	LEU	A	917	26.165	12.061	45.884	1.00	20.00
6246	CD1	LEU	A	917	25.876	13.041	47.022	1.00	21.86
6247	CD2	LEU	A	917	24.848	11.880	45.129	1.00	20.00
6248	N	ILE	A	918	28.502	9.935	46.675	1.00	16.06
6249	CA	ILE	A	918	28.452	8.487	46.780	1.00	16.89
6250	C	ILE	A	918	27.272	8.137	47.700	1.00	18.66
6251	O	ILE	A	918	27.097	8.663	48.785	1.00	16.20
6252	CB	ILE	A	918	29.732	7.784	47.268	1.00	17.77
6253	CG1	ILE	A	918	30.930	8.148	46.370	1.00	18.54
6254	CG2	ILE	A	918	29.487	6.275	47.309	1.00	17.76
6255	CD1	ILE	A	918	32.249	7.494	46.754	1.00	20.20
6256	N	LEU	A	919	26.369	7.351	47.131	1.00	21.26
6257	CA	LEU	A	919	25.184	6.865	47.783	1.00	27.90
6258	C	LEU	A	919	25.295	5.346	47.929	1.00	30.33
6259	O	LEU	A	919	25.969	4.669	47.164	1.00	32.18
6260	CB	LEU	A	919	23.770	7.282	47.400	1.00	25.84
6261	CG	LEU	A	919	23.523	8.755	47.030	1.00	24.77
6262	CD1	LEU	A	919	22.135	8.877	46.388	1.00	25.08
6263	CD2	LEU	A	919	23.622	9.633	48.256	1.00	24.26
6264	N	LYS	A	920	24.551	4.859	48.938	1.00	36.42
6265	CA	LYS	A	920	24.617	3.434	49.196	1.00	43.04
6266	C	LYS	A	920	23.193	3.022	49.576	1.00	45.32
6267	1OCT	LYS	A	920	22.398	3.801	51.035	1.00	45.54
6268	CB	LYS	A	920	25.523	2.759	50.280	1.00	44.65
6269	CG	LYS	A	920	24.968	2.992	51.689	1.00	44.34
6270	CD	LYS	A	920	25.851	2.376	52.776	1.00	20.00
6271	CE	LYS	A	920	25.377	2.731	54.189	1.00	20.00
6272	NZ	LYS	A	920	25.874	1.739	55.139	1.00	20.00
6273	N	GLN	A	921	22.682	1.858	49.773	1.00	20.00
6274	CA	GLN	A	921	21.286	1.476	50.372	1.00	20.00
6275	C	GLN	A	921	21.261	0.073	50.618	1.00	20.00
6276	O	GLN	A	921	22.159	-0.710	50.334	1.00	20.00
6277	CB	GLN	A	921	19.846	1.531	49.828	1.00	20.00
6278	CG	GLN	A	921	19.352	2.234	48.564	1.00	20.00
6279	CD	GLN	A	921	18.079	1.727	47.929	1.00	20.00
6280	OE1	GLN	A	921	17.783	0.808	47.183	1.00	20.00
6281	NE2	GLN	A	921	17.165	2.459	48.597	1.00	20.00
6282	OW0	WAT	W	68	69.366	-6.548	12.439	1.00	14.02
6283	OW0	WAT	W	69	32.120	-4.756	50.871	1.00	13.28
6284	OW0	WAT	W	70	81.609	-10.422	31.503	1.00	15.09
6285	OW0	WAT	W	71	62.367	-0.879	37.668	1.00	12.62
6286	OW0	WAT	W	73	68.913	-12.263	29.623	1.00	13.17
6287	OW0	WAT	W	74	48.063	10.500	38.858	1.00	11.72
6288	OW0	WAT	W	75	32.559	-7.482	50.485	1.00	13.66
6289	OW0	WAT	W	76	32.469	1.638	38.626	1.00	14.80
6290	OW0	WAT	W	77	65.428	-1.416	31.925	1.00	11.95
6291	OW0	WAT	W	78	48.212	16.412	42.613	1.00	20.28
6292	OW0	WAT	W	79	57.789	3.719	36.390	1.00	12.67
6293	OW0	WAT	W	80	75.360	-12.767	22.439	1.00	15.67
6294	OW0	WAT	W	81	61.875	-3.084	20.619	1.00	17.60
6295	OW0	WAT	W	82	60.223	-2.292	27.508	1.00	11.71
6296	OW0	WAT	W	83	73.802	-6.472	17.967	1.00	11.91
6297	OW0	WAT	W	84	63.768	4.437	40.319	1.00	13.88
6298	OW0	WAT	W	85	36.975	5.299	53.120	1.00	17.10
6299	OW0	WAT	W	86	33.546	14.270	46.569	1.00	19.57
6300	OW0	WAT	W	87	59.158	9.717	41.808	1.00	15.61
6301	OW0	WAT	W	88	41.880	-1.805	42.672	1.00	18.22
6302	OW0	WAT	W	89	56.275	9.738	41.533	1.00	13.72
6303	OW0	WAT	W	90	69.059	-23.930	9.758	1.00	20.01
6304	OW0	WAT	W	91	16.344	1.857	52.326	1.00	22.62
6305	OW0	WAT	W	92	75.875	-9.053	49.382	1.00	20.09
6306	OW0	WAT	W	93	76.720	-4.117	4.820	1.00	19.57
6307	OW0	WAT	W	94	32.604	16.958	29.686	1.00	15.11
6308	OW0	WAT	W	95	14.139	7.588	47.083	1.00	18.86
6309	OW0	WAT	W	96	39.342	-8.437	34.765	1.00	18.36
6310	OW0	WAT	W	97	53.612	13.510	41.564	1.00	15.07
6311	OW0	WAT	W	98	36.908	-3.575	37.657	1.00	16.19
6312	OW0	WAT	W	99	81.997	-19.278	2.244	1.00	21.87
6313	OW0	WAT	W	100	34.008	1.090	27.119	1.00	17.80
6314	OW0	WAT	W	101	56.888	19.001	45.064	1.00	16.05
6315	OW0	WAT	W	102	31.113	8.775	55.007	1.00	16.75
6316	OW0	WAT	W	103	68.763	-13.614	32.213	1.00	14.83
6317	OW0	WAT	W	104	77.576	-15.120	38.787	1.00	17.30
6318	OW0	WAT	W	105	70.975	9.008	41.415	1.00	15.80
6319	OW0	WAT	W	106	73.071	8.260	45.444	1.00	19.77
6320	OW0	WAT	W	107	29.643	15.604	46.570	1.00	15.52
6321	OW0	WAT	W	108	77.037	-3.080	44.844	1.00	17.45
6322	OW0	WAT	W	109	71.489	-9.613	39.434	1.00	14.35
6323	OW0	WAT	W	110	41.593	-4.442	45.963	1.00	18.94
6324	OW0	WAT	W	111	63.736	-11.016	10.939	1.00	17.44
6325	OW0	WAT	W	112	40.024	2.255	37.806	1.00	13.52
6326	OW0	WAT	W	113	64.610	-1.339	34.837	1.00	14.96
6327	OW0	WAT	W	114	61.987	20.548	50.028	1.00	19.83
6328	OW0	WAT	W	115	72.528	-7.124	29.593	1.00	18.15
6329	OW0	WAT	W	116	47.271	-11.141	34.789	1.00	18.03
6330	OW0	WAT	W	117	50.553	17.125	41.460	1.00	18.99
6331	OW0	WAT	W	118	54.956	14.273	35.671	1.00	17.04
6332	OW0	WAT	W	119	22.721	16.885	49.692	1.00	18.22
6333	OW0	WAT	W	120	68.820	9.178	39.628	1.00	15.40

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6334	OWO	WAT	W	121	58.258	13.263	29.566	1.00	17.29
6335	OWO	WAT	W	122	51.860	-6.953	40.625	1.00	16.39
6336	OWO	WAT	W	123	24.503	9.804	33.921	1.00	16.52
6337	OWO	WAT	W	124	82.641	-4.698	41.936	1.00	23.28
6338	OWO	WAT	W	125	81.955	-8.160	8.351	1.00	24.39
6339	OWO	WAT	W	126	62.535	5.308	26.770	1.00	21.48
6340	OWO	WAT	W	127	46.588	-10.586	39.440	1.00	17.61
6341	OWO	WAT	W	128	60.874	11.097	38.475	1.00	15.05
6342	OWO	WAT	W	129	79.219	-10.342	12.004	1.00	17.14
6343	OWO	WAT	W	130	75.096	-14.661	24.693	1.00	15.31
6344	OWO	WAT	W	131	37.686	29.364	40.600	1.00	21.16
6345	OWO	WAT	W	132	67.581	0.034	15.638	1.00	16.05
6346	OWO	WAT	W	133	70.269	1.088	49.178	1.00	14.16
6347	OWO	WAT	W	134	77.523	-12.820	37.177	1.00	13.66
6348	OWO	WAT	W	135	77.079	-2.476	26.781	1.00	22.54
6349	OWO	WAT	W	136	44.250	-9.198	31.555	1.00	19.30
6350	OWO	WAT	W	137	43.079	26.840	29.301	1.00	23.07
6351	OWO	WAT	W	138	73.331	-7.883	32.692	1.00	14.37
6352	OWO	WAT	W	139	70.346	8.134	44.604	1.00	19.57
6353	OWO	WAT	W	140	47.819	9.959	23.729	1.00	19.80
6354	OWO	WAT	W	141	48.447	-8.906	33.755	1.00	15.32
6355	OWO	WAT	W	142	29.592	15.853	27.070	1.00	25.10
6356	OWO	WAT	W	143	45.897	-14.006	-16.368	1.00	21.95
6357	OWO	WAT	W	144	65.522	5.063	38.083	1.00	12.12
6358	OWO	WAT	W	145	67.211	0.550	32.731	1.00	17.01
6359	OWO	WAT	W	146	58.188	15.032	33.459	1.00	18.00
6360	OWO	WAT	W	147	56.888	-10.260	18.807	1.00	24.03
6361	OWO	WAT	W	148	69.862	-15.067	24.194	1.00	12.26
6362	OWO	WAT	W	149	66.848	18.769	50.441	1.00	26.40
6363	OWO	WAT	W	150	39.850	10.596	24.937	1.00	15.47
6364	OWO	WAT	W	151	46.212	-0.290	-4.537	1.00	19.55
6365	OWO	WAT	W	152	69.349	10.471	29.638	1.00	25.61
6366	OWO	WAT	W	153	75.556	-7.180	31.034	1.00	17.73
6367	OWO	WAT	W	154	77.494	-24.179	15.886	1.00	19.43
6368	OWO	WAT	W	155	62.259	12.967	49.436	1.00	16.99
6369	OWO	WAT	W	157	81.536	-10.806	5.685	1.00	17.76
6370	OWO	WAT	W	158	62.854	-16.944	21.280	1.00	30.32
6371	OWO	WAT	W	159	47.815	-3.762	-20.195	1.00	24.16
6372	OWO	WAT	W	160	74.332	-2.627	26.574	1.00	20.89
6373	OWO	WAT	W	161	73.134	-8.343	11.701	1.00	14.37
6374	OWO	WAT	W	162	35.562	-10.370	30.256	1.00	16.76
6375	OWO	WAT	W	163	89.451	-13.445	20.007	1.00	17.74
6376	OWO	WAT	W	164	64.437	-8.353	11.350	1.00	19.87
6377	OWO	WAT	W	165	42.448	-1.014	52.692	1.00	25.22
6378	OWO	WAT	W	166	46.191	-7.466	32.597	1.00	19.58
6379	OWO	WAT	W	167	74.558	-4.139	51.689	1.00	21.48
6380	OWO	WAT	W	168	58.355	12.098	38.036	1.00	18.33
6381	OWO	WAT	W	169	64.827	20.010	32.662	1.00	24.95
6382	OWO	WAT	W	170	46.993	18.543	20.841	1.00	20.41
6383	OWO	WAT	W	171	35.631	21.698	36.640	1.00	16.68
6384	OWO	WAT	W	172	54.527	4.577	34.040	1.00	16.16
6385	OWO	WAT	W	173	79.048	-13.312	16.275	1.00	19.28
6386	OWO	WAT	W	174	34.755	5.781	57.522	1.00	28.62
6387	OWO	WAT	W	175	24.290	-8.263	41.358	1.00	27.30
6388	OWO	WAT	W	176	43.005	20.391	32.602	1.00	20.84
6389	OWO	WAT	W	177	30.870	-2.649	54.736	1.00	25.48
6390	OWO	WAT	W	178	53.261	8.959	50.601	1.00	24.03
6391	OWO	WAT	W	179	53.517	5.558	31.784	1.00	24.92
6392	OWO	WAT	W	180	68.153	-15.586	16.468	1.00	17.73
6393	OWO	WAT	W	181	80.333	-14.549	-8.414	1.00	28.75
6394	OWO	WAT	W	182	77.155	4.046	42.470	1.00	16.63
6395	OWO	WAT	W	183	36.194	17.220	43.863	1.00	17.32
6396	OWO	WAT	W	184	74.883	3.842	36.360	1.00	18.34
6397	OWO	WAT	W	185	43.383	31.022	45.350	1.00	34.65
6398	OWO	WAT	W	186	55.792	6.996	60.761	1.00	19.70
6399	OWO	WAT	W	187	62.221	10.100	60.967	1.00	17.41
6400	OWO	WAT	W	188	72.467	-14.137	23.905	1.00	18.11
6401	OWO	WAT	W	189	43.775	-10.296	29.108	1.00	13.72
6402	OWO	WAT	W	190	46.321	8.776	37.734	1.00	17.82
6403	OWO	WAT	W	191	58.197	4.756	57.467	1.00	18.48
6404	OWO	WAT	W	192	18.946	19.472	50.053	1.00	43.73
6405	OWO	WAT	W	193	46.641	23.645	40.314	1.00	15.11
6406	OWO	WAT	W	194	73.073	2.447	2.145	1.00	25.40
6407	OWO	WAT	W	195	69.006	20.130	42.674	1.00	29.03
6408	OWO	WAT	W	196	68.843	-18.109	15.825	1.00	22.65
6409	OWO	WAT	W	197	18.045	9.415	37.687	1.00	23.22
6410	OWO	WAT	W	198	19.821	3.539	53.564	1.00	25.47
6411	OWO	WAT	W	199	37.934	-8.358	42.258	1.00	22.96
6412	OWO	WAT	W	200	66.324	-17.028	33.133	1.00	21.67
6413	OWO	WAT	W	201	89.568	-0.730	43.526	1.00	39.85
6414	OWO	WAT	W	202	65.791	-8.953	56.239	1.00	24.77
6415	OWO	WAT	W	203	30.336	-3.688	-15.714	1.00	31.23
6416	OWO	WAT	W	204	38.412	2.069	31.675	1.00	14.46
6417	OWO	WAT	W	205	48.840	-16.134	30.302	1.00	22.40
6418	OWO	WAT	W	206	66.776	20.286	40.341	1.00	25.65
6419	OWO	WAT	W	207	37.823	3.881	27.553	1.00	16.42
6420	OWO	WAT	W	208	51.918	25.040	45.285	1.00	35.74
6421	OWO	WAT	W	209	57.850	21.185	46.630	1.00	23.05
6422	OWO	WAT	W	210	20.044	17.034	49.140	1.00	14.24
6423	OWO	WAT	W	211	71.715	-5.894	10.737	1.00	16.38
6424	OWO	WAT	W	212	66.725	-5.950	11.424	1.00	25.24
6425	OWO	WAT	W	213	69.977	-19.080	28.620	1.00	22.47
6426	OWO	WAT	W	214	41.220	-1.629	45.498	1.00	14.57
6427	OWO	WAT	W	215	80.849	-10.168	9.676	1.00	15.11
6428	OWO	WAT	W	216	65.460	-4.423	5.582	1.00	25.44
6429	OWO	WAT	W	217	60.371	3.984	54.712	1.00	19.11

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6430	OW0	WAT	W	218	46.146	-14.480	-19.119	1.00	22.68
6431	OW0	WAT	W	220	75.425	-5.678	28.718	1.00	14.44
6432	OW0	WAT	W	221	64.613	5.872	48.455	1.00	15.74
6433	OW0	WAT	W	222	76.468	4.175	45.089	1.00	15.34
6434	OW0	WAT	W	223	78.530	-3.248	30.018	1.00	18.35
6435	OW0	WAT	W	224	66.447	-15.601	45.227	1.00	21.57
6436	OW0	WAT	W	225	64.601	13.864	43.344	1.00	19.79
6437	OW0	WAT	W	226	84.129	-21.451	40.447	1.00	23.07
6438	OW0	WAT	W	227	50.240	9.246	25.360	1.00	27.34
6439	OW0	WAT	W	228	71.340	-3.838	2.003	1.00	28.41
6440	OW0	WAT	W	229	85.282	-20.669	0.886	1.00	31.69
6441	OW0	WAT	W	230	26.568	-10.850	46.117	1.00	21.74
6442	OW0	WAT	W	231	70.878	-18.207	31.358	1.00	23.68
6443	OW0	WAT	W	232	35.309	24.294	36.012	1.00	20.39
6444	OW0	WAT	W	233	52.580	4.977	18.388	1.00	22.44
6445	OW0	WAT	W	234	50.557	11.295	58.608	1.00	20.04
6446	OW0	WAT	W	235	23.949	20.846	34.191	1.00	26.29
6447	OW0	WAT	W	236	35.623	14.411	43.636	1.00	19.95
6448	OW0	WAT	W	237	64.405	-7.438	8.777	1.00	24.16
6449	OW0	WAT	W	238	75.075	-15.366	34.214	1.00	24.35
6450	OW0	WAT	W	239	49.008	-14.858	26.445	1.00	18.45
6451	OW0	WAT	W	240	67.130	18.121	47.777	1.00	26.38
6452	OW0	WAT	W	241	58.462	-8.275	-6.771	1.00	27.46
6453	OW0	WAT	W	242	89.032	-3.538	32.201	1.00	37.77
6454	OW0	WAT	W	243	76.413	-9.886	12.043	1.00	19.59
6455	OW0	WAT	W	244	91.058	-23.122	27.002	1.00	29.55
6456	OW0	WAT	W	245	68.897	-16.420	32.353	1.00	17.73
6457	OW0	WAT	W	246	60.787	20.118	45.579	1.00	19.06
6458	OW0	WAT	W	247	57.295	9.602	38.862	1.00	18.19
6459	OW0	WAT	W	248	51.834	13.502	33.252	1.00	16.33
6460	OW0	WAT	W	250	37.078	29.140	45.806	1.00	19.44
6461	OW0	WAT	W	251	79.365	-4.623	6.311	1.00	27.30
6462	OW0	WAT	W	252	50.994	3.684	58.665	1.00	26.14
6463	OW0	WAT	W	253	16.237	1.326	45.058	1.00	21.57
6464	OW0	WAT	W	254	59.347	18.360	43.822	1.00	21.00
6465	OW0	WAT	W	255	93.718	-8.612	37.885	1.00	27.72
6466	OW0	WAT	W	256	18.476	13.116	37.804	1.00	20.53
6467	OW0	WAT	W	257	74.988	-1.264	7.841	1.00	23.15
6468	OW0	WAT	W	258	65.708	-9.485	2.882	1.00	24.47
6469	OW0	WAT	W	259	81.228	-18.556	15.613	1.00	21.70
6470	OW0	WAT	W	260	40.153	18.506	50.014	1.00	29.11
6471	OW0	WAT	W	261	76.275	-15.000	27.216	1.00	14.07
6472	OW0	WAT	W	262	32.653	-11.672	30.238	1.00	24.10
6473	OW0	WAT	W	263	33.719	19.637	32.612	1.00	23.35
6474	OW0	WAT	W	264	57.975	6.308	29.825	1.00	28.17
6475	OW0	WAT	W	265	56.014	3.037	13.415	1.00	27.45
6476	OW0	WAT	W	266	35.289	-10.133	-21.987	1.00	24.36
6477	OW0	WAT	W	267	48.772	-1.478	-18.710	1.00	22.08
6478	OW0	WAT	W	268	56.907	-15.816	-21.447	1.00	21.69
6479	OW0	WAT	W	269	70.103	-9.623	56.538	1.00	21.05
6480	OW0	WAT	W	270	66.182	8.595	31.274	1.00	23.04
6481	OW0	WAT	W	271	43.509	-7.089	-19.497	1.00	25.51
6482	OW0	WAT	W	272	75.559	-23.596	13.036	1.00	25.28
6483	OW0	WAT	W	273	52.581	11.622	50.505	1.00	19.81
6484	OW0	WAT	W	274	70.407	-23.742	7.358	1.00	26.46
6485	OW0	WAT	W	275	47.060	18.265	28.697	1.00	32.17
6486	OW0	WAT	W	276	45.135	20.614	54.368	1.00	26.24
6487	OW0	WAT	W	277	78.588	-20.221	12.456	1.00	28.74
6488	OW0	WAT	W	278	26.272	-3.352	44.999	1.00	18.45
6489	OW0	WAT	W	279	27.844	23.521	45.472	1.00	19.15
6490	OW0	WAT	W	280	43.415	-9.483	-20.814	1.00	22.24
6491	OW0	WAT	W	281	44.928	-9.823	21.085	1.00	21.62
6492	OW0	WAT	W	282	67.718	4.640	5.963	1.00	25.19
6493	OW0	WAT	W	283	96.982	-10.458	37.245	1.00	30.81
6494	OW0	WAT	W	284	48.457	4.929	-7.033	1.00	23.97
6495	OW0	WAT	W	285	55.985	-7.377	-3.129	1.00	27.03
6496	OW0	WAT	W	286	35.786	-2.048	0.183	1.00	30.57
6497	OW0	WAT	W	287	78.219	-5.390	40.921	1.00	16.49
6498	OW0	WAT	W	288	77.364	-21.161	31.334	1.00	18.15
6499	OW0	WAT	W	289	50.808	-19.872	31.259	1.00	23.98
6500	OW0	WAT	W	290	31.863	-12.519	43.355	1.00	21.97
6501	OW0	WAT	W	291	49.112	-1.399	15.411	1.00	32.14
6502	OW0	WAT	W	292	36.747	2.739	53.684	1.00	28.77
6503	OW0	WAT	W	293	47.932	-3.952	50.396	1.00	29.44
6504	OW0	WAT	W	294	75.259	-18.091	42.038	1.00	27.99
6505	OW0	WAT	W	295	65.026	17.315	32.530	1.00	25.64
6506	OW0	WAT	W	296	78.244	-25.283	12.611	1.00	35.84
6507	OW0	WAT	W	297	85.182	-4.003	27.099	1.00	38.09
6508	OW0	WAT	W	298	58.707	-10.508	52.943	1.00	20.88
6509	OW0	WAT	W	299	51.111	17.227	31.022	1.00	29.87
6510	OW0	WAT	W	300	61.340	-13.950	17.572	1.00	27.41
6511	OW0	WAT	W	301	38.209	-3.845	-22.771	1.00	26.19
6512	OW0	WAT	W	302	72.914	-22.668	6.220	1.00	26.26
6513	OW0	WAT	W	303	66.840	-21.476	4.405	1.00	27.43
6514	OW0	WAT	W	304	50.616	-5.935	44.803	1.00	18.59
6515	OW0	WAT	W	305	77.962	12.398	43.121	1.00	32.94
6516	OW0	WAT	W	306	66.149	-13.682	-12.914	1.00	28.81
6517	OW0	WAT	W	307	82.412	-2.518	2.943	1.00	26.24
6518	OW0	WAT	W	308	37.840	23.041	26.322	1.00	28.62
6519	OW0	WAT	W	309	61.723	-12.439	11.952	1.00	27.68
6520	OW0	WAT	W	310	45.805	-15.302	29.600	1.00	42.22
6521	OW0	WAT	W	311	37.738	11.900	54.333	1.00	30.73
6522	OW0	WAT	W	312	78.463	-14.147	-10.311	1.00	23.91
6523	OW0	WAT	W	313	46.583	-15.364	34.986	1.00	23.46
6524	OW0	WAT	W	314	62.766	5.097	12.438	1.00	22.65
6525	OW0	WAT	W	315	43.230	0.820	-21.984	1.00	35.81

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6526	OW0	WAT	W	316	43.950	4.358	-15.650	1.00	23.67
6527	OW0	WAT	W	317	42.859	-10.546	45.639	1.00	32.28
6528	OW0	WAT	W	318	49.162	-3.978	1.765	1.00	43.38
6529	OW0	WAT	W	319	60.903	21.253	54.960	1.00	32.40
6530	OW0	WAT	W	320	84.179	-7.984	18.419	1.00	21.93
6531	OW0	WAT	W	321	44.701	-15.753	-5.792	1.00	24.15
6532	OW0	WAT	W	322	17.649	6.695	35.037	1.00	33.00
6533	OW0	WAT	W	323	39.424	-10.529	42.109	1.00	24.43
6534	OW0	WAT	W	324	17.053	-3.033	44.924	1.00	32.20
6535	OW0	WAT	W	325	71.659	-19.394	34.189	1.00	39.67
6536	OW0	WAT	W	326	60.464	-11.885	54.688	1.00	29.00
6537	OW0	WAT	W	327	60.150	8.501	29.954	1.00	22.12
6538	OW0	WAT	W	328	71.908	12.459	33.945	1.00	31.00
6539	OW0	WAT	W	329	50.518	-6.710	-4.970	1.00	24.35
6540	OW0	WAT	W	330	81.378	-2.927	27.039	1.00	28.44
6541	OW0	WAT	W	331	69.282	-16.298	45.601	1.00	27.45
6542	OW0	WAT	W	332	67.427	-13.423	-6.333	1.00	30.02
6543	OW0	WAT	W	333	46.329	-12.182	37.298	1.00	20.51
6544	OW0	WAT	W	334	48.718	-20.006	-14.082	1.00	29.70
6545	OW0	WAT	W	335	43.754	-13.207	36.811	1.00	26.82
6546	OW0	WAT	W	336	64.098	14.236	26.166	1.00	29.05
6547	OW0	WAT	W	337	37.049	3.266	-19.372	1.00	31.08
6548	OW0	WAT	W	338	61.795	-10.158	-4.790	1.00	34.78
6549	OW0	WAT	W	339	49.037	0.420	51.729	1.00	23.15
6550	OW0	WAT	W	340	75.001	-18.929	4.449	1.00	25.65
6551	OW0	WAT	W	341	65.358	-16.321	0.957	1.00	30.48
6552	OW0	WAT	W	342	42.464	13.861	23.091	1.00	28.92
6553	OW0	WAT	W	343	88.313	-2.838	44.183	1.00	29.50
6554	OW0	WAT	W	344	32.606	12.506	24.842	1.00	22.59
6555	OW0	WAT	W	345	56.691	16.693	46.428	1.00	23.81
6556	OW0	WAT	W	346	91.741	-3.418	41.436	1.00	31.63
6557	OW0	WAT	W	347	41.803	11.235	23.103	1.00	38.16
6558	OW0	WAT	W	348	46.070	-13.919	32.782	1.00	29.90
6559	OW0	WAT	W	349	54.505	-7.501	-20.473	1.00	30.31
6560	OW0	WAT	W	350	80.666	-8.291	47.313	1.00	31.98
6561	OW0	WAT	W	351	72.442	3.961	-1.194	1.00	29.66
6562	OW0	WAT	W	352	37.415	6.655	27.782	1.00	26.05
6563	OW0	WAT	W	353	68.123	-17.644	51.248	1.00	32.02
6564	OW0	WAT	W	354	61.089	23.461	40.340	1.00	27.24
6565	OW0	WAT	W	355	19.026	-6.909	51.121	1.00	26.68
6566	OW0	WAT	W	356	34.952	4.204	-5.390	1.00	33.99
6567	OW0	WAT	W	357	44.994	-11.459	33.261	1.00	25.35
6568	OW0	WAT	W	358	45.207	-6.145	46.236	1.00	25.52
6569	OW0	WAT	W	360	40.573	15.286	24.984	1.00	28.94
6570	OW0	WAT	W	361	72.962	2.265	55.757	1.00	26.75
6571	OW0	WAT	W	362	71.459	-26.046	4.160	1.00	28.61
6572	OW0	WAT	W	363	38.402	20.036	48.661	1.00	22.55
6573	OW0	WAT	W	364	32.615	21.884	33.926	1.00	31.74
6574	OW0	WAT	W	365	80.451	-4.586	48.849	1.00	25.59
6575	OW0	WAT	W	366	73.839	-20.204	6.685	1.00	23.97
6576	OW0	WAT	W	367	79.652	-24.057	29.577	1.00	25.40
6577	OW0	WAT	W	368	49.566	13.147	31.160	1.00	38.08
6578	OW0	WAT	W	369	38.584	8.766	23.418	1.00	24.62
6579	OW0	WAT	W	370	77.248	-23.896	30.696	1.00	25.85
6580	OW0	WAT	W	371	77.989	-20.493	8.093	1.00	28.17
6581	OW0	WAT	W	372	47.120	-18.023	33.871	1.00	30.24
6582	OW0	WAT	W	373	10.465	5.660	47.993	1.00	36.55
6583	OW0	WAT	W	374	57.307	14.254	27.302	1.00	27.17
6584	OW0	WAT	W	375	38.985	13.275	24.929	1.00	23.57
6585	OW0	WAT	W	376	72.047	-16.693	37.366	1.00	32.15
6586	OW0	WAT	W	377	47.471	4.237	-17.052	1.00	36.00
6587	OW0	WAT	W	378	51.129	-18.579	-13.092	1.00	23.58
6588	OW0	WAT	W	379	86.696	-24.221	18.981	1.00	29.96
6589	OW0	WAT	W	380	85.791	-0.516	37.710	1.00	29.15
6590	OW0	WAT	W	381	84.814	-13.838	11.838	1.00	25.35
6591	OW0	WAT	W	382	28.157	-11.801	44.088	1.00	22.15
6592	OW0	WAT	W	383	62.926	22.843	35.656	1.00	35.59
6593	OW0	WAT	W	384	17.572	0.721	42.711	1.00	18.81
6594	OW0	WAT	W	385	75.014	-27.098	16.437	1.00	25.43
6595	OW0	WAT	W	386	67.132	-16.141	-2.946	1.00	32.78
6596	OW0	WAT	W	387	22.477	9.654	59.781	1.00	34.92
6597	OW0	WAT	W	388	28.624	-2.581	27.502	1.00	40.90
6598	OW0	WAT	W	389	68.480	5.583	25.870	1.00	20.19
6599	OW0	WAT	W	390	72.335	-15.678	52.469	1.00	24.90
6600	OW0	WAT	W	391	72.401	9.938	47.835	1.00	38.08
6601	OW0	WAT	W	392	37.136	-4.896	3.579	1.00	39.22
6602	OW0	WAT	W	393	87.130	-3.587	22.928	1.00	28.96
6603	OW0	WAT	W	394	59.733	21.534	42.236	1.00	19.04
6604	OW0	WAT	W	395	49.614	-6.092	47.633	1.00	26.38
6605	OW0	WAT	W	396	68.508	-18.979	0.775	1.00	25.22
6606	OW0	WAT	W	397	30.344	16.345	53.767	1.00	21.53
6607	OW0	WAT	W	398	36.689	-10.063	44.341	1.00	27.75
6608	OW0	WAT	W	399	44.255	10.317	20.950	1.00	38.55
6609	OW0	WAT	W	400	80.351	-27.377	31.973	1.00	29.96
6610	OW0	WAT	W	401	62.323	-7.884	-10.201	1.00	25.19
6611	OW0	WAT	W	402	48.124	-18.230	-10.307	1.00	28.48
6612	OW0	WAT	W	403	61.453	-14.796	-18.703	1.00	40.45
6613	OW0	WAT	W	404	66.241	-21.530	28.934	1.00	30.44
6614	OW0	WAT	W	405	39.152	22.713	47.906	1.00	17.90
6615	OW0	WAT	W	406	46.042	-16.832	-9.093	1.00	35.13
6616	OW0	WAT	W	407	63.039	0.557	60.763	1.00	33.78
6617	OW0	WAT	W	408	64.512	10.494	17.998	1.00	31.21
6618	OW0	WAT	W	409	66.376	-17.542	55.784	1.00	21.41
6619	OW0	WAT	W	410	47.053	-15.752	-6.786	1.00	27.55
6620	OW0	WAT	W	411	25.339	-10.076	43.114	1.00	23.49
6621	OW0	WAT	W	412	66.204	-5.949	25.409	1.00	30.80

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6622	OWO	WAT	W	413	38.412	-12.030	33.503	1.00	27.23
6623	OWO	WAT	W	414	33.850	28.896	42.331	1.00	47.21
6624	OWO	WAT	W	415	17.795	16.340	37.828	1.00	33.59
6625	OWO	WAT	W	416	34.565	-12.132	-23.818	1.00	31.86
6626	OWO	WAT	W	417	91.832	-14.160	17.359	1.00	37.03
6627	OWO	WAT	W	418	47.439	14.844	32.551	1.00	33.39
6628	OWO	WAT	W	419	69.434	-25.542	21.203	1.00	41.60
6629	OWO	WAT	W	420	55.830	-14.109	41.979	1.00	51.22
6630	OWO	WAT	W	421	42.926	-12.881	34.347	1.00	23.83
6631	OWO	WAT	W	422	63.743	-0.676	4.790	1.00	36.35
6632	OWO	WAT	W	423	55.526	0.391	11.719	1.00	43.19
6633	OWO	WAT	W	424	73.417	12.097	49.004	1.00	38.46
6634	OWO	WAT	W	425	52.369	24.730	35.218	1.00	28.92
6635	OWO	WAT	W	426	62.668	-12.567	-11.718	1.00	28.63
6636	OWO	WAT	W	427	64.528	-14.519	-11.603	1.00	34.77
6637	OWO	WAT	W	428	85.369	-26.700	28.869	1.00	34.96
6638	OWO	WAT	W	429	34.890	11.971	56.023	1.00	30.32
6639	OWO	WAT	W	430	38.319	13.761	52.914	1.00	38.81
6640	OWO	WAT	W	431	36.205	-3.725	22.946	1.00	38.51
6641	OWO	WAT	W	432	61.755	-18.698	19.722	1.00	32.41
6642	OWO	WAT	W	433	73.740	-17.674	33.635	1.00	36.99
6643	OWO	WAT	W	434	62.176	-18.812	26.590	1.00	35.56
6644	OWO	WAT	W	435	80.166	-4.065	15.814	1.00	41.24
6645	OWO	WAT	W	436	63.537	-3.108	10.225	1.00	26.01
6646	OWO	WAT	W	437	70.855	11.063	55.846	1.00	38.80
6647	OWO	WAT	W	438	55.025	19.284	36.156	1.00	21.38
6648	OWO	WAT	W	439	82.953	-0.517	19.836	1.00	31.57
6649	OWO	WAT	W	440	77.688	3.005	35.260	1.00	27.61
6650	OWO	WAT	W	441	47.174	-19.776	-25.723	1.00	25.70
6651	OWO	WAT	W	442	15.282	-0.724	48.333	1.00	63.95
6652	OWO	WAT	W	443	45.668	2.364	56.289	1.00	29.20
6653	OWO	WAT	W	444	55.704	7.505	11.701	1.00	31.83
6654	OWO	WAT	W	445	41.558	6.741	55.087	1.00	34.44
6655	OWO	WAT	W	446	73.701	7.136	28.230	1.00	26.54
6656	OWO	WAT	W	447	21.624	11.628	31.608	1.00	30.60
6657	OWO	WAT	W	448	97.126	-16.727	30.310	1.00	34.64
6658	OWO	WAT	W	449	74.340	-4.743	24.963	1.00	45.37
6659	OWO	WAT	W	450	84.402	-6.560	16.139	1.00	30.72
6660	OWO	WAT	W	451	28.262	21.244	24.604	1.00	43.08
6661	OWO	WAT	W	452	23.084	1.809	31.647	1.00	26.48
6662	OWO	WAT	W	453	42.394	-4.193	3.333	1.00	31.81
6663	OWO	WAT	W	454	62.371	-1.473	8.394	1.00	27.83
6664	OWO	WAT	W	455	46.837	6.251	21.345	1.00	36.13
6665	OWO	WAT	W	456	35.480	26.992	45.795	1.00	28.88
6666	OWO	WAT	W	457	51.976	-7.138	-1.858	1.00	31.75
6667	OWO	WAT	W	458	69.604	-18.226	42.817	1.00	31.57
6668	OWO	WAT	W	459	68.233	-16.493	-13.125	1.00	34.37
6669	OWO	WAT	W	460	38.919	4.604	-15.945	1.00	30.77
6670	OWO	WAT	W	461	54.603	-1.784	-10.268	1.00	29.83
6671	OWO	WAT	W	462	75.522	-18.796	38.966	1.00	35.67
6672	OWO	WAT	W	463	81.655	-2.401	17.151	1.00	32.07
6673	OWO	WAT	W	464	57.826	-19.166	25.096	1.00	38.97
6674	OWO	WAT	W	465	81.263	-20.540	14.119	1.00	33.94
6675	OWO	WAT	W	466	63.386	-6.403	6.370	1.00	39.46
6676	OWO	WAT	W	467	81.257	0.044	-1.327	1.00	37.79
6677	OWO	WAT	W	468	46.062	-15.455	-25.516	1.00	41.40
6678	OWO	WAT	W	469	20.247	20.109	38.622	1.00	27.65
6679	OWO	WAT	W	470	77.490	-21.509	14.231	1.00	36.26
6680	OWO	WAT	W	471	76.196	-24.636	0.276	1.00	43.65
6681	OWO	WAT	W	472	30.399	24.885	35.289	1.00	33.93
6682	OWO	WAT	W	473	30.055	13.347	25.308	1.00	32.70
6683	OWO	WAT	W	474	84.910	-4.142	0.423	1.00	39.08
6684	OWO	WAT	W	475	31.259	0.007	-12.949	1.00	31.64
6685	OWO	WAT	W	476	36.835	26.993	49.651	1.00	27.17
6686	OWO	WAT	W	477	90.488	-25.441	33.765	1.00	38.84
6687	OWO	WAT	W	478	58.971	15.316	62.875	1.00	38.57
6688	OWO	WAT	W	479	71.338	-25.348	1.040	1.00	55.72
6689	OWO	WAT	W	480	41.705	-19.415	-13.619	1.00	37.68
6690	OWO	WAT	W	481	69.730	14.867	50.512	1.00	26.27
6691	OWO	WAT	W	482	14.828	13.346	51.319	1.00	27.62
6692	OWO	WAT	W	483	90.856	-21.318	-3.133	1.00	53.86
6693	OWO	WAT	W	484	56.183	-9.627	16.617	1.00	30.41
6694	OWO	WAT	W	485	57.382	-1.553	-6.767	1.00	29.36
6695	OWO	WAT	W	486	37.727	-6.554	-23.027	1.00	31.09
6696	OWO	WAT	W	487	60.051	24.897	33.921	1.00	48.03
6697	OWO	WAT	W	488	17.634	15.818	50.213	1.00	46.53
6698	OWO	WAT	W	489	78.778	-24.898	44.836	1.00	40.33
6699	OWO	WAT	W	490	65.719	9.772	60.623	1.00	47.51
6700	OWO	WAT	W	491	21.583	-9.599	41.401	1.00	37.21
6701	OWO	WAT	W	492	47.040	2.603	20.841	1.00	34.24
6702	OWO	WAT	W	493	54.279	1.535	-18.697	1.00	44.41
6703	OWO	WAT	W	494	62.066	-1.934	-8.477	1.00	39.01
6704	OWO	WAT	W	495	30.722	-7.382	-7.418	1.00	34.70
6705	OWO	WAT	W	496	31.310	1.784	-6.926	1.00	31.46
6706	OWO	WAT	W	497	52.330	11.012	30.962	1.00	32.49
6707	OWO	WAT	W	498	65.945	-20.083	21.418	1.00	30.34
6708	OWO	WAT	W	499	50.770	-10.173	12.866	1.00	47.95
6709	OWO	WAT	W	500	61.046	23.935	37.360	1.00	32.34
6710	OWO	WAT	W	501	39.600	2.991	-0.996	1.00	46.45
6711	OWO	WAT	W	502	27.724	-11.311	40.533	1.00	16.56
6712	OWO	WAT	W	503	59.536	-2.849	-8.699	1.00	28.34
6713	OWO	WAT	W	504	40.735	24.000	49.923	1.00	34.03
6714	OWO	WAT	W	505	73.997	-27.214	14.115	1.00	43.47
6715	OWO	WAT	W	506	40.887	-10.965	33.589	1.00	26.99
6716	OWO	WAT	W	507	82.531	3.559	45.765	1.00	30.67
6717	OWO	WAT	W	508	48.547	-17.731	-5.638	1.00	44.65

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6718	OWO	WAT	W	509	40.883	-5.002	48.490	1.00	31.16
6719	OWO	WAT	W	510	76.430	-25.387	32.925	1.00	30.36
6720	OWO	WAT	W	511	71.990	12.764	51.191	1.00	30.30
6721	OWO	WAT	W	512	20.681	0.962	54.358	1.00	33.83
6722	OWO	WAT	W	513	27.139	25.062	36.224	1.00	39.95
6723	OWO	WAT	W	514	83.997	-20.448	13.120	1.00	46.83
6724	OWO	WAT	W	515	79.230	-24.653	37.743	1.00	35.45
6725	OWO	WAT	W	516	38.032	-10.688	-25.566	1.00	31.11
6726	OWO	WAT	W	517	88.040	-1.843	36.126	1.00	30.26
6727	OWO	WAT	W	518	71.250	15.795	48.528	1.00	29.38
6728	OWO	WAT	W	520	15.848	7.343	57.167	1.00	32.22
6729	OWO	WAT	W	521	34.398	-21.215	-9.737	1.00	44.50
6730	OWO	WAT	W	522	64.038	-6.164	54.619	1.00	32.76
6731	OWO	WAT	W	523	64.354	1.072	-3.179	1.00	29.78
6732	OWO	WAT	W	524	85.120	3.839	36.045	1.00	40.08
6733	OWO	WAT	W	525	86.257	2.953	41.138	1.00	41.59
6734	OWO	WAT	W	526	52.892	6.449	29.807	1.00	29.56
6735	OWO	WAT	W	527	44.099	5.976	-11.549	1.00	27.68
6736	OWO	WAT	W	528	54.883	-0.564	-7.820	1.00	28.79
6737	OWO	WAT	W	529	80.659	-25.958	36.000	1.00	43.82
6738	OWO	WAT	W	530	77.061	-1.218	13.093	1.00	33.25
6739	OWO	WAT	W	531	12.960	2.681	41.428	1.00	40.30
6740	OWO	WAT	W	532	15.085	14.951	49.204	1.00	33.19
6741	OWO	WAT	W	533	66.186	-17.851	36.224	1.00	44.47
6742	OWO	WAT	W	534	33.556	-7.708	-22.528	1.00	36.36
6743	OWO	WAT	W	535	64.789	-11.150	5.378	1.00	30.63
6744	OWO	WAT	W	536	60.271	6.086	27.464	1.00	32.06
6745	OWO	WAT	W	537	90.487	-15.669	14.264	1.00	35.70
6746	OWO	WAT	W	538	79.423	-0.659	26.417	1.00	32.62
6747	OWO	WAT	W	539	27.499	-9.225	41.241	1.00	38.84
6748	OWO	WAT	W	540	38.460	-17.144	-22.854	1.00	32.97
6749	OWO	WAT	W	541	95.109	-18.447	21.117	1.00	45.20
6750	OWO	WAT	W	542	46.885	1.862	-21.845	1.00	45.25
6751	OWO	WAT	W	543	72.300	15.489	37.082	1.00	38.81
6752	OWO	WAT	W	544	53.484	-19.303	24.437	1.00	31.94
6753	OWO	WAT	W	545	68.271	-16.075	53.457	1.00	33.31
6754	OWO	WAT	W	546	81.187	-12.562	8.492	1.00	31.48
6755	OWO	WAT	W	547	49.103	-15.891	43.116	1.00	33.62
6756	OWO	WAT	W	548	63.252	-20.824	18.880	1.00	38.97
6757	OWO	WAT	W	549	86.032	-2.093	25.031	1.00	38.83
6758	OWO	WAT	W	550	50.812	-9.392	-2.366	1.00	32.70
6759	OWO	WAT	W	551	77.222	-22.310	5.262	1.00	42.02
6760	OWO	WAT	W	552	87.105	0.417	40.246	1.00	33.75
6761	OWO	WAT	W	553	39.779	-10.913	28.103	1.00	32.23
6762	OWO	WAT	W	554	80.530	5.700	44.684	1.00	22.37
6763	OWO	WAT	W	555	44.445	21.933	51.741	1.00	40.68
6764	OWO	WAT	W	556	78.037	4.895	33.580	1.00	38.94
6765	OWO	WAT	W	557	50.785	-1.091	53.731	1.00	40.29
6766	OWO	WAT	W	558	48.427	-18.608	31.494	1.00	38.93
6767	OWO	WAT	W	559	36.861	8.729	55.912	1.00	32.41
6768	OWO	WAT	W	560	34.764	8.292	57.897	1.00	41.50
6769	OWO	WAT	W	561	52.719	-18.428	-15.193	1.00	34.83
6770	OWO	WAT	W	562	21.141	21.506	43.413	1.00	35.68
6771	OWO	WAT	W	563	32.675	10.931	22.641	1.00	33.70
6772	OWO	WAT	W	564	79.498	-28.457	28.133	1.00	41.72
6773	OWO	WAT	W	565	31.047	-13.425	34.555	1.00	32.76
6774	OWO	WAT	W	566	17.333	-4.663	51.771	1.00	23.15
6775	OWO	WAT	W	567	73.981	-25.793	-1.995	1.00	46.66
6776	OWO	WAT	W	568	54.933	7.887	31.452	1.00	35.09
6777	OWO	WAT	W	569	40.812	-13.172	37.899	1.00	34.36
6778	OWO	WAT	W	570	90.118	-22.677	43.385	1.00	42.30
6779	OWO	WAT	W	571	49.795	16.333	32.935	1.00	33.34
6780	OWO	WAT	W	572	86.224	-3.103	29.568	1.00	45.18
6781	OWO	WAT	W	573	93.985	-21.583	25.927	1.00	49.38
6782	OWO	WAT	W	574	48.711	29.216	31.209	1.00	38.64
6783	OWO	WAT	W	575	80.779	-26.481	29.557	1.00	41.33
6784	OWO	WAT	W	576	30.291	-0.331	-3.469	1.00	33.78
6785	OWO	WAT	W	577	83.004	-7.012	12.342	1.00	54.12
6786	OWO	WAT	W	578	77.402	10.589	36.940	1.00	34.01
6787	OWO	WAT	W	579	36.261	17.002	46.660	1.00	36.83
6788	OWO	WAT	W	580	72.862	13.977	47.223	1.00	31.19
6789	OWO	WAT	W	581	47.939	-15.855	24.111	1.00	32.81
6790	OWO	WAT	W	582	77.692	6.100	24.255	1.00	39.63
6791	OWO	WAT	W	583	64.653	-13.766	4.879	1.00	38.84
6792	OWO	WAT	W	584	46.486	-2.333	51.867	1.00	65.57
6793	OWO	WAT	W	585	76.557	6.773	47.617	1.00	30.60
6794	OWO	WAT	W	586	55.689	0.519	60.810	1.00	37.55
6795	OWO	WAT	W	587	77.597	-7.073	50.855	1.00	34.75
6796	OWO	WAT	W	588	88.395	-13.032	11.580	1.00	29.59
6797	OWO	WAT	W	589	41.920	18.111	24.362	1.00	32.25
6798	OWO	WAT	W	590	37.249	-12.482	31.297	1.00	28.69
6799	OWO	WAT	W	591	82.022	-21.727	0.851	1.00	41.41
6800	OWO	WAT	W	592	74.315	9.720	29.056	1.00	36.96
6801	OWO	WAT	W	593	51.410	5.026	-6.751	1.00	40.52
6802	OWO	WAT	W	594	47.526	10.717	59.474	1.00	44.35
6803	OWO	WAT	W	595	53.540	-15.820	20.692	1.00	36.01
6804	OWO	WAT	W	596	34.459	-9.657	26.624	1.00	33.62
6805	OWO	WAT	W	597	67.159	18.723	29.650	1.00	47.65
6806	OWO	WAT	W	598	57.902	-6.416	11.043	1.00	36.87
6807	OWO	WAT	W	599	33.150	10.072	56.599	1.00	36.61
6808	OWO	WAT	W	600	80.247	-13.720	45.923	1.00	38.71
6809	OWO	WAT	W	601	65.256	5.486	60.044	1.00	25.49
6810	OWO	WAT	W	602	70.764	-21.357	-4.897	1.00	34.79
6811	OWO	WAT	W	603	43.485	-13.298	22.439	1.00	36.93
6812	OWO	WAT	W	604	55.370	23.838	31.451	1.00	40.61
6813	OWO	WAT	W	605	72.230	-4.477	53.756	1.00	33.63

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6814	OW0	WAT	W	606	86.015	-6.308	44.482	1.00	33.31
6815	OW0	WAT	W	607	79.100	6.742	28.261	1.00	36.39
6816	OW0	WAT	W	608	13.024	10.093	41.592	1.00	39.66
6817	OW0	WAT	W	610	19.065	2.738	56.666	1.00	36.22
6818	OW0	WAT	W	611	27.698	18.474	28.229	1.00	29.78
6819	OW0	WAT	W	612	79.524	-22.097	-5.261	1.00	35.00
6820	OW0	WAT	W	613	78.777	3.843	-0.369	1.00	39.60
6821	OW0	WAT	W	614	60.674	23.492	32.021	1.00	50.31
6822	OW0	WAT	W	615	89.369	-13.520	6.901	1.00	53.93
6823	OW0	WAT	W	616	54.674	2.066	-7.514	1.00	35.44
6824	OW0	WAT	W	617	80.241	-21.114	10.183	1.00	45.60
6825	OW0	WAT	W	618	39.869	-0.368	53.204	1.00	31.86
6826	OW0	WAT	W	619	84.314	0.222	22.029	1.00	38.74
6827	OW0	WAT	W	620	77.764	-28.451	25.257	1.00	42.43
6828	OW0	WAT	W	621	92.860	-6.918	29.400	1.00	43.50
6829	OW0	WAT	W	623	82.066	-22.011	-5.845	1.00	43.27
6830	OW0	WAT	W	624	66.952	21.443	36.324	1.00	35.06
6831	OW0	WAT	W	625	65.091	-21.080	25.542	1.00	36.11
6832	OW0	WAT	W	626	95.260	-15.509	41.378	1.00	32.64
6833	OW0	WAT	W	627	60.917	-1.177	-13.410	1.00	40.04
6834	OW0	WAT	W	628	60.376	-14.353	56.761	1.00	47.88
6835	OW0	WAT	W	629	35.528	-17.752	-20.354	1.00	38.18
6836	OW0	WAT	W	630	53.084	17.303	25.669	1.00	46.68
6837	OW0	WAT	W	631	49.338	24.584	23.434	1.00	37.08
6838	OW0	WAT	W	632	44.633	31.369	41.827	1.00	51.68
6839	OW0	WAT	W	633	41.364	9.274	55.363	1.00	48.19
6840	OW0	WAT	W	634	85.480	-8.670	45.623	1.00	38.50
6841	OW0	WAT	W	635	67.366	8.090	27.660	1.00	46.28
6842	OW0	WAT	W	636	58.044	20.208	61.858	1.00	43.81
6843	OW0	WAT	W	637	60.247	-6.665	-19.077	1.00	33.84
6844	OW0	WAT	W	638	22.729	2.441	55.615	1.00	38.38
6845	OW0	WAT	W	639	58.636	-8.488	-2.049	1.00	45.41
6846	OW0	WAT	W	640	51.765	-5.454	-24.427	1.00	30.07
6847	OW0	WAT	W	641	60.477	-7.078	-5.334	1.00	51.94
6848	OW0	WAT	W	642	35.217	24.951	48.021	1.00	36.69
6849	OW0	WAT	W	643	25.477	8.964	26.926	1.00	36.50
6850	OW0	WAT	W	644	73.038	7.145	25.686	1.00	38.10
6851	OW0	WAT	W	645	31.546	26.839	42.458	1.00	37.72
6852	OW0	WAT	W	646	78.629	5.276	46.680	1.00	31.14
6853	OW0	WAT	W	647	50.352	-10.415	0.030	1.00	34.69
6854	OW0	WAT	W	648	23.075	3.622	57.785	1.00	50.55
6855	OW0	WAT	W	649	82.155	-23.495	3.245	1.00	34.51
6856	OW0	WAT	W	650	53.614	-0.820	-5.533	1.00	30.46
6857	OW0	WAT	W	651	41.173	6.120	-12.244	1.00	32.87
6858	OW0	WAT	W	652	46.461	15.785	29.821	1.00	33.74
6859	OW0	WAT	W	653	46.910	-0.266	53.614	1.00	36.78
6860	OW0	WAT	W	654	54.969	9.457	27.413	1.00	41.28
6861	OW0	WAT	W	655	71.413	4.824	11.859	1.00	47.81
6862	OW0	WAT	W	656	48.713	3.240	-19.259	1.00	36.50
6863	OW0	WAT	W	657	53.539	25.302	32.981	1.00	38.05
6864	OW0	WAT	W	658	53.590	-1.475	8.457	1.00	51.45
6865	OW0	WAT	W	659	79.662	-22.479	-0.183	1.00	50.01
6866	OW0	WAT	W	660	18.141	15.650	34.789	1.00	53.01
6867	OW0	WAT	W	661	87.154	-0.180	42.783	1.00	47.33
6868	OW0	WAT	W	662	62.459	9.375	29.050	1.00	30.93
6869	OW0	WAT	W	663	42.984	25.814	49.065	1.00	34.72
6870	OW0	WAT	W	664	89.832	-5.536	43.041	1.00	35.89
6871	OW0	WAT	W	666	95.356	-6.463	30.956	1.00	39.83
6872	OW0	WAT	W	667	70.567	14.899	27.721	1.00	47.74
6873	OW0	WAT	W	668	38.060	1.861	56.019	1.00	43.81
6874	OW0	WAT	W	669	42.573	-12.553	29.782	1.00	44.56
6875	OW0	WAT	W	670	63.052	-18.013	29.178	1.00	32.11
6876	OW0	WAT	W	671	26.904	-12.528	-19.449	1.00	50.32
6877	OW0	WAT	W	672	87.381	-14.602	9.308	1.00	38.68
6878	OW0	WAT	W	673	73.626	-6.763	27.221	1.00	44.79
6879	OW0	WAT	W	674	19.297	10.427	29.648	1.00	53.79
6880	OW0	WAT	W	675	61.974	-17.776	43.690	1.00	45.64
6881	OW0	WAT	W	676	21.734	16.509	28.603	1.00	52.65
6882	OW0	WAT	W	677	90.154	-12.035	4.840	1.00	52.27
6883	OW0	WAT	W	678	77.008	5.083	18.362	1.00	38.43
6884	OW0	WAT	W	679	78.849	-3.340	8.660	1.00	44.26
6885	OW0	WAT	W	680	37.125	6.546	25.017	1.00	26.76
6886	OW0	WAT	W	681	65.476	13.560	57.511	1.00	38.57
6887	OW0	WAT	W	682	54.416	3.948	15.578	1.00	40.81
6888	OW0	WAT	W	683	53.062	-18.088	22.008	1.00	43.19
6889	OW0	WAT	W	684	12.292	12.538	42.132	1.00	32.07
6890	OW0	WAT	W	685	22.880	9.102	31.205	1.00	44.59
6891	OW0	WAT	W	686	24.576	-0.920	55.112	1.00	42.14
6892	OW0	WAT	W	687	61.965	-4.738	11.865	1.00	34.12
6893	OW0	WAT	W	688	54.878	-16.136	18.394	1.00	42.78
6894	OW0	WAT	W	689	16.847	19.568	45.126	1.00	43.60
6895	OW0	WAT	W	690	55.170	23.039	52.155	1.00	41.75
6896	OW0	WAT	W	691	39.834	-12.044	-3.476	1.00	36.25
6897	OW0	WAT	W	692	83.900	-19.454	48.185	1.00	42.85
6898	OW0	WAT	W	693	62.276	19.955	30.431	1.00	34.17
6899	OW0	WAT	W	694	84.970	-6.738	10.835	1.00	42.23
6900	OW0	WAT	W	695	35.725	-14.462	31.165	1.00	39.86
6901	OW0	WAT	W	696	58.055	17.975	63.613	1.00	53.19
6902	OW0	WAT	W	697	48.858	27.436	43.339	1.00	47.28
6903	OW0	WAT	W	698	63.336	-8.234	57.236	1.00	47.00
6904	OW0	WAT	W	699	70.147	-26.087	29.342	1.00	55.27
6905	OW0	WAT	W	700	66.692	-14.096	-16.368	1.00	45.91
6906	OW0	WAT	W	701	40.692	15.224	56.764	1.00	46.42
6907	OW0	WAT	W	702	79.719	-28.791	22.760	1.00	32.02
6908	OW0	WAT	W	703	59.465	21.759	30.551	1.00	42.42
6909	OW0	WAT	W	704	31.141	-5.131	22.552	1.00	68.52

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6910	OWO	WAT	W	705	36.695	-16.973	-4.878	1.00	37.89
6911	OWO	WAT	W	706	80.687	-20.765	47.298	1.00	38.30
6912	OWO	WAT	W	707	54.669	3.010	-9.815	1.00	46.05
6913	OWO	WAT	W	708	43.216	-8.260	47.123	1.00	40.03
6914	OWO	WAT	W	709	70.862	15.600	41.973	1.00	37.00
6915	OWO	WAT	W	710	33.412	-2.522	54.114	1.00	48.11
6916	OWO	WAT	W	711	92.535	-0.923	34.738	1.00	49.47
6917	OWO	WAT	W	712	33.025	23.917	47.317	1.00	46.24
6918	OWO	WAT	W	713	70.249	17.850	37.204	1.00	40.78
6919	OWO	WAT	W	714	41.368	22.495	53.675	1.00	40.32
6920	OWO	WAT	W	715	76.578	-19.899	49.657	1.00	40.87
6921	OWO	WAT	W	716	90.425	-4.420	30.203	1.00	60.30
6922	OWO	WAT	W	717	34.487	19.062	20.833	1.00	45.89
6923	OWO	WAT	W	718	89.801	-4.016	22.869	1.00	46.61
6924	OWO	WAT	W	719	74.377	1.047	-13.486	1.00	51.80
6925	OWO	WAT	W	720	66.403	4.257	9.718	1.00	41.97
6926	OWO	WAT	W	721	56.444	-17.979	-12.402	1.00	40.83
6927	OWO	WAT	W	722	82.588	-0.182	1.654	1.00	55.22
6928	OWO	WAT	W	723	61.949	-0.825	-0.993	1.00	44.85
6929	OWO	WAT	W	724	94.665	-3.882	41.279	1.00	43.45
6930	OWO	WAT	W	725	78.637	-22.418	46.944	1.00	49.42
6931	OWO	WAT	W	726	76.801	0.776	11.150	1.00	43.15
6932	OWO	WAT	W	727	36.682	26.179	34.703	1.00	46.16
6933	OWO	WAT	W	728	52.946	-24.152	35.886	1.00	42.32
6934	OWO	WAT	W	729	44.065	-10.820	0.741	1.00	58.49
6935	OWO	WAT	W	730	59.442	-15.580	42.690	1.00	31.69
6936	OWO	WAT	W	731	72.384	8.537	51.566	1.00	31.82
6937	OWO	WAT	W	732	31.347	-6.053	26.265	1.00	42.64
6938	OWO	WAT	W	733	34.630	6.679	23.929	1.00	43.41
6939	OWO	WAT	W	734	57.088	-11.759	-15.829	1.00	40.44
6940	OWO	WAT	W	735	79.179	-22.870	6.833	1.00	45.12
6941	OWO	WAT	W	736	38.310	-14.037	35.139	1.00	44.86
6942	OWO	WAT	W	737	39.171	-2.907	53.911	1.00	45.60
6943	OWO	WAT	W	738	39.322	17.940	52.385	1.00	42.20
6944	OWO	WAT	W	739	48.359	2.635	58.769	1.00	51.66
6945	OWO	WAT	W	740	72.823	5.269	52.825	1.00	45.87
6946	OWO	WAT	W	741	52.762	19.727	28.434	1.00	40.22
6947	OWO	WAT	W	742	28.202	-5.793	-6.513	1.00	48.77
6948	OWO	WAT	W	743	79.618	1.235	4.432	1.00	42.94
6949	OWO	WAT	W	744	67.094	-18.257	47.501	1.00	38.02
6950	OWO	WAT	W	745	52.688	10.357	62.956	1.00	40.29
6951	OWO	WAT	W	746	40.431	-14.509	-4.481	1.00	42.77
6952	OWO	WAT	W	747	38.750	-10.992	22.885	1.00	44.88
6953	OWO	WAT	W	748	44.292	14.402	59.454	1.00	44.70
6954	OWO	WAT	W	749	88.953	-23.063	20.219	1.00	41.34
6955	OWO	WAT	W	750	56.054	-11.968	53.046	1.00	60.38
6956	OWO	WAT	W	751	41.969	29.748	47.846	1.00	20.50
6957	OWO	WAT	W	752	44.966	-16.181	23.899	1.00	50.48
6958	OWO	WAT	W	753	85.644	-22.932	2.568	1.00	43.55
6959	OWO	WAT	W	754	43.034	6.314	-21.514	1.00	51.86
6960	OWO	WAT	W	755	84.872	4.181	42.842	1.00	49.44
6961	OWO	WAT	W	756	74.363	11.696	34.959	1.00	37.97
6962	OWO	WAT	W	757	80.803	5.977	33.052	1.00	43.23
6963	OWO	WAT	W	758	61.280	17.301	58.888	1.00	40.96
6964	OWO	WAT	W	759	35.859	19.793	23.282	1.00	48.10
6965	OWO	WAT	W	760	20.148	19.237	32.614	1.00	31.76
6966	OWO	WAT	W	761	15.289	11.762	36.214	1.00	43.45
6967	OWO	WAT	W	762	46.595	-5.917	-22.133	1.00	44.31
6968	OWO	WAT	W	763	20.413	11.283	60.057	1.00	50.11
6969	OWO	WAT	W	764	68.167	5.712	13.653	1.00	30.67
6970	OWO	WAT	W	765	54.184	2.615	-12.252	1.00	39.38
6971	OWO	WAT	W	766	84.664	-22.555	14.359	1.00	45.78
6972	OWO	WAT	W	767	30.072	-20.212	-10.959	1.00	38.35
6973	OWO	WAT	W	768	41.072	-0.946	-21.837	1.00	41.66
6974	OWO	WAT	W	769	61.874	11.916	27.798	1.00	44.81
6975	OWO	WAT	W	770	66.356	5.178	-1.773	1.00	65.15
6976	OWO	WAT	W	771	26.844	5.186	59.968	1.00	46.27
6977	OWO	WAT	W	772	36.878	24.305	28.318	1.00	34.70
6978	OWO	WAT	W	773	54.912	-1.550	-21.819	1.00	42.64
6979	OWO	WAT	W	774	59.594	-17.858	41.366	1.00	37.27
6980	OWO	WAT	W	775	57.520	-15.150	18.294	1.00	36.30
6981	OWO	WAT	W	776	32.998	24.523	34.342	1.00	42.23
6982	OWO	WAT	W	777	59.020	-12.114	56.789	1.00	57.61
6983	OWO	WAT	W	778	81.113	-27.278	43.621	1.00	41.79
6984	OWO	WAT	W	779	73.319	-20.756	38.654	1.00	43.17
6985	OWO	WAT	W	780	75.478	-16.566	37.845	1.00	51.42
6986	OWO	WAT	W	781	91.610	-6.042	15.770	1.00	36.38
6987	OWO	WAT	W	782	71.605	16.644	39.410	1.00	48.62
6988	OWO	WAT	W	783	63.508	24.207	41.029	1.00	44.22
6989	OWO	WAT	W	784	88.822	-11.109	7.822	1.00	48.78
6990	OWO	WAT	W	785	71.691	-23.906	33.801	1.00	48.29
6991	OWO	WAT	W	786	52.032	8.913	29.301	1.00	39.41
6992	OWO	WAT	W	787	72.141	14.023	31.846	1.00	37.55
6993	OWO	WAT	W	788	39.138	16.149	26.862	1.00	50.27
6994	OWO	WAT	W	789	37.813	-9.039	47.875	1.00	13.18
6995	OWO	WAT	W	790	35.173	-8.363	50.198	1.00	39.87
6996	OWO	WAT	W	791	26.847	-1.258	31.548	1.00	39.21
6997	OWO	WAT	W	792	88.614	-23.766	1.624	1.00	54.25
6998	OWO	WAT	W	793	21.121	7.089	31.169	1.00	50.12
6999	OWO	WAT	W	794	41.636	21.622	50.969	1.00	47.76
7000	OWO	WAT	W	795	26.421	0.362	29.613	1.00	43.60
7001	OWO	WAT	W	796	44.401	-8.843	-23.747	1.00	40.62
7002	OWO	WAT	W	797	70.057	18.053	42.138	1.00	38.55
7003	OWO	WAT	W	798	66.270	-17.604	-6.916	1.00	45.58
7004	OWO	WAT	W	799	46.164	31.367	45.417	1.00	51.35
7005	OWO	WAT	W	800	75.137	5.508	51.679	1.00	45.47

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7006	OWO	WAT	W	801	18.046	3.941	59.147	1.00	42.23
7007	OWO	WAT	W	802	59.339	0.402	-2.076	1.00	52.88
7008	OWO	WAT	W	803	55.564	-18.287	-15.179	1.00	38.85
7009	OWO	WAT	W	804	28.418	0.009	26.267	1.00	52.59
7010	OWO	WAT	W	805	97.132	-12.269	27.826	1.00	38.21
7011	OWO	WAT	W	806	21.485	21.769	33.106	1.00	37.99
7012	OWO	WAT	W	807	61.494	-16.277	-11.458	1.00	32.24
7013	OWO	WAT	W	808	77.944	-0.349	8.828	1.00	56.65
7014	OWO	WAT	W	809	75.983	-17.170	-12.760	1.00	35.83
7015	OWO	WAT	W	810	52.665	-11.955	-2.121	1.00	42.38
7016	OWO	WAT	W	811	54.291	-1.443	-1.785	1.00	38.65
7017	OWO	WAT	W	812	51.272	6.345	31.812	1.00	46.84
7018	OWO	WAT	W	813	96.248	-8.528	40.673	1.00	36.47
7019	OWO	WAT	W	814	21.883	-7.783	54.051	1.00	37.11
7020	OWO	WAT	W	815	41.687	30.174	33.806	1.00	43.95
7021	OWO	WAT	W	816	49.364	-19.438	-8.102	1.00	46.98
7022	OWO	WAT	W	817	63.992	20.309	53.102	1.00	38.77
7023	OWO	WAT	W	818	65.323	12.002	26.726	1.00	45.31
7024	OWO	WAT	W	819	44.245	-15.998	36.333	1.00	36.72
7025	OWO	WAT	W	820	61.512	-12.703	-20.772	1.00	42.86
7026	OWO	WAT	W	821	40.874	-3.535	-22.568	1.00	37.17
7027	OWO	WAT	W	822	53.950	22.361	28.394	1.00	48.45
7028	OWO	WAT	W	823	47.488	6.176	-13.884	1.00	39.21
7029	OWO	WAT	W	824	62.078	-1.860	61.143	1.00	48.06
7030	OWO	WAT	W	825	83.442	-26.335	2.633	1.00	59.67
7031	OWO	WAT	W	826	82.792	-0.371	24.014	1.00	41.82
7032	OWO	WAT	W	827	49.672	12.353	60.988	1.00	43.87
7033	OWO	WAT	W	828	41.022	-7.720	48.703	1.00	39.62
7034	OWO	WAT	W	829	64.480	1.533	-6.989	1.00	39.53
7035	OWO	WAT	W	830	19.350	12.831	57.326	1.00	35.73
7036	OWO	WAT	W	831	22.229	14.191	30.825	1.00	54.08
7037	OWO	WAT	W	832	69.924	16.102	52.996	1.00	35.01
7038	OWO	WAT	W	833	80.371	-18.513	48.901	1.00	45.56
7039	OWO	WAT	W	834	64.966	-13.780	2.163	1.00	45.15
7040	OWO	WAT	W	835	90.651	-7.000	22.378	1.00	39.28
7041	OWO	WAT	W	836	70.311	5.553	14.709	1.00	31.82
7042	OWO	WAT	W	837	45.088	24.790	51.597	1.00	50.96
7043	OWO	WAT	W	838	65.259	23.437	36.483	1.00	58.46
7044	OWO	WAT	W	839	23.969	-18.104	-13.469	1.00	44.45
7045	OWO	WAT	W	840	98.275	-11.384	39.798	1.00	40.16
7046	OWO	WAT	W	841	43.468	-4.550	50.159	1.00	42.27
7047	OWO	WAT	W	842	55.531	24.997	41.758	1.00	43.49
7048	OWO	WAT	W	843	79.423	-25.689	-0.377	1.00	50.83
7049	OWO	WAT	W	844	82.729	-5.447	14.530	1.00	37.55
7050	OWO	WAT	W	845	57.277	-20.688	32.754	1.00	27.47
7051	OWO	WAT	W	846	34.927	18.980	47.765	1.00	43.87
7052	OWO	WAT	W	847	66.697	21.490	33.750	1.00	55.52
7053	OWO	WAT	W	848	52.866	-18.940	42.635	1.00	48.02
7054	OWO	WAT	W	849	50.290	-12.920	19.561	1.00	49.79
7055	OWO	WAT	W	850	24.446	5.767	29.203	1.00	39.68
7056	OWO	WAT	W	851	44.555	9.373	55.910	1.00	30.53
7057	OWO	WAT	W	852	59.190	7.201	65.033	1.00	43.41
7058	OWO	WAT	W	853	23.010	7.765	61.451	1.00	52.83
7059	OWO	WAT	W	854	22.922	24.189	36.031	1.00	41.20
7060	OWO	WAT	W	855	57.790	-3.694	56.332	1.00	51.83
7061	OWO	WAT	W	856	23.937	14.064	59.101	1.00	46.09
7062	OWO	WAT	W	857	65.116	20.932	49.254	1.00	41.13
7063	OWO	WAT	W	858	38.488	17.732	55.214	1.00	40.12
7064	OWO	WAT	W	859	39.060	7.114	-23.052	1.00	31.07
7065	OWO	WAT	W	860	44.261	9.954	-10.440	1.00	45.44
7066	OWO	WAT	W	861	57.678	24.011	45.961	1.00	35.78
7067	OWO	WAT	W	862	62.731	-18.645	24.010	1.00	34.48
7068	OWO	WAT	W	863	55.872	23.413	49.005	1.00	52.80
7069	OWO	WAT	W	864	78.578	2.825	2.653	1.00	47.81
7070	OWO	WAT	W	865	82.130	-6.162	9.951	1.00	45.86
7071	OWO	WAT	W	866	69.803	-18.155	38.558	1.00	50.20
7072	OWO	WAT	W	867	11.916	7.726	43.912	1.00	34.68
END				867	11.916	7.726	43.912	1.00	34.68

APPENDIX 1

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             1                                                     50
Promozyme    DSTSTKVIVH YHRFDSNYTN WDVWMWPYQP VNGNGAAYQF TGTNDDFGAV
B.acidopul   DSTSTEVIVH YHRFDSNYAN WDLWMWPYQP VNGNGAAYEF SG.KDDFGVK
B.deramifi   DGNTTTIIVH YFRPAGDYQP WSLWMW...P KDGGGAEYDF NQPADSFGAV

             51                                                   100
Promozyme    ADTQVPGDNT QVGLIVRKND WSEKNTPNDL HIDLAKGHEV WIVQGDPTIY
B.acidopul   ADVQVPGDDT QVGLIVRTND WSQKNTSDDL HIDLTKGHEI WIVQGDPNIY
B.deramifi   ASADIPGNPS QVGIIVRTQD WT.KDVSADR YIDLSKGNEV WLVEGNSQIF

             101                                                  150
Promozyme    YNLSDAQAAA IPSVSNAYLD DEKTVLAKLS MPMTLADAAS GFTVIDKTTG
B.acidopul   YNLSDAQAAA TPKVSNAYLD NEKTVLAKLT NPMTLSDGSS GFTVTDKTTG
B.deramifi   YNEKDAEDAA KPAVSNAYLD ASNQVLVKLS QPLTLGEGAS GFTVHDDTAN

             151                                                  197
Promozyme    EKIPVTSAVS A...NPVTAV LVGDLQQALG AANNWSPDDD HTLLKKINPN
B.acidopul   EQIPVTAATN A...NS.... .......... .......... ..........
B.deramifi   KDIPVTSVKD ASLGQDVTAV LAGTFQHIFG GS.DWAPDNH STLLKKVTNN

             198                                                  246
Promozyme    LYQLSGTLPA GTYQYKIALD HSW.NTSYPG NNVSLTVPQG GEKVTFTYIP
B.acidopul   .......... .......... .......... .......... ..........
B.deramifi   LYQFSGDLPE GNYQYKVALN DSWNNPSYPS DNINLTVPAG GAHVTFSYIP

             247                                                  296
Promozyme    STNQVFDSVN HPNQAFPTSS AGVQTNLVQL TLASAPDVTH NLDVAADGYK
B.acidopul   .......... ........AS SSEQTDLVQL TLASAPDVSH TIQVGAAGYE
B.deramifi   STHAVYDTIN NPNADLQVES .GVKTDLVTV TLGEDPDVSH TLSIQTDGYQ

             297                                                  346
Promozyme    AHNILPRNVL NLPRYDYSGN DLGNVYSKDA TSFRVWAPTA SNVQLLLYNS
B.acidopul   AVNLIPRNVL NLPRYYYSGN DLGNVYSNKA TAFRVWAPTA SDVQLLLYNS
B.deramifi   AKQVIPRNVL NSSQYYYSGD DLGNTYTQKA TTFKVWAPTS TQVNVLLYDS

             347                                                  396
Promozyme    EKGSITKQLE MQKSDNGTWK LQVSGNLENW YYLYQVTVNG TTQTAVDPYA
B.acidopul   ETGPVTKQLE MQKSDNGTWK LKVPGNLKNW YYLYQVTVNG KTQTAVDPYV
B.deramifi   ATGSVTKIVP MTASGHGVWE ATVNQNLENW YYMYEVTGQG STRTAVDPYA

             397                                                  446
Promozyme    RAISVNATRG MIVDLKATDP AGWQGDHEQT PANPVDEVIY EAHVRDFSID
B.acidopul   RAISVNATRG MIVDLEDTNP PGWKEDHQQT PANPVDEVIY EVHVRDFSID
B.deramifi   TAIAPNGTRG MIVDLAKTDP AGWNSDKHIT PKNIEDEVIY EMDVRDFSID

             447                                                  496
Promozyme    ANSGMKNKGK YLAFTEHGTK GPDHVKTGID SLKELGITTV QLQPVEEFNS
B.acidopul   ANSGMKNKGK YLAFTEHGTK GPDNVKTGID SLKELGINAV QLQPIEEFNS
B.deramifi   PNSGMKNKGK YLALTEKGTK GPDNVKTGID SLKQLGITHV QLMPVFASNS

             497                                                  546
Promozyme    IDETQPDTYN WGYDPRNYNV PEGAYATTPE GTARITELKQ LIQSLHQQRI
B.acidopul   IDETQPNMYN WGYDPRNYNV PEGAYATTPE GTARITQLKQ LIQSIHKDRI
B.deramifi   VDETDPTQDN WGYDPRNYDV PEGQYATNAN GNARIKEFKE MVLSLHREHI
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APPENDIX 2

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            547                                                      596
Promozyme   GVNMDVVYNH TFDVMVSDFD KIVPQYYYRT DSNGNYTNGS GCGNEFATEH
B.acidopul  AINMDVVYNH TFNVGVSDFD KIVPQYYYRT DSAGNYTNGS GVGNEIATER
B.deramifi  GVNMDVVYNH TFATQISDFD KIVPEYYYRT DDAGNYTNGS GTGNEIAAER

            597                                                      646
Promozyme   PMAQKFVLDS VNYWVNEYHV DGFRFDLMAL LGKDTMAKIS NELHAINPGI
B.acidopul  PMVQKFVLDS VKYWVKEYHI DGFRFDLMAL LGKDTMAKIS KELHAINPGI
B.deramifi  PMVQKFIIDS LKYWVNEYHI DGFRFDLMAL LGKDTMSKAA SELHAINPGI

            647                                                      696
Promozyme   VLYGEPWTGG TSGLSSDQLV TKGQQKGLGI GVFNDNIRNG LDGNVFDKTA
B.acidopul  VLYGEPWTGG TSGLSSDQLV TKGQQKGLGI GVFNDNIRNG LDGNVFDKSA
B.deramifi  ALYGEPWTGG TSALPDDQLL TKGAQKGMGV AVFNDNLRNA LDGNVFDSSA

            697                                                      746
Promozyme   QGFATGDPNQ VDVIKNGVIG SIQDFTSAPS ETINYVTSHD NMTLWDKILA
B.acidopul  QGFATGDPNQ VNVIKNRVMG SISDFTSAPS ETINYVTSHD NMTLWDKISA
B.deramifi  QGFATGATGL TDAIKNGVEG SINDFTSSPG ETINYVTSHD NYTLWDKIAL

            747                                                      796
Promozyme   SNPSDTEADR IKMDELAHAV VFTSQGVPFM QGGEEMLRTK GGNDNSYNAG
B.acidopul  SNPNDTQADR IKMDELAQAV VFTSQGVPFM QGGEEMLRTK GGNDNSYNAG
B.deramifi  SNPNDSEADR IKMDELAQAV VMTSQGVPFM QGGEEMLRTK GGNDNSYNAG

            797                                                      846
Promozyme   DSVNQFDWSR KAQFKDVFDY FSSMIHLRNQ HPAFRMTTAD QIKQNLTFLE
B.acidopul  DSVNQFDWSR KAQFENVFDY YSWLIHLRDN HPAFRMTTAD QIKQNLTFLD
B.deramifi  DAVNEFDWSR KAQYPDVFNY YSGLIHLRLD HPAFRMTTAN EINSHLQFLN

            847                                                      896
Promozyme   SPTNTVAFEL KNYANHDTWK NIIVMYNPNK TSQTLNLPSG DWTIVGLGDQ
B.acidopul  SPTNTVAFEL KNHANHDKWK NIIVMYNPNK TAQTLTLPSG NWTIVGLGNQ
B.deramifi  SPENTVAYEL TDHVNKDKWG NIIVVYNPNK TVATINLPSG KWAINATSGK

            897                   921
Promozyme   IGEKSLGHVM GNVQVPAIST LILKQ..... .....
B.acidopul  VGEKSLGHVN GTVEVPALST IILHQGTSED VIDQN
B.deramifi  VGESTLGQAE GSVQVPGISM MILHQEVSPD HGKK.
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APPENDIX 2